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Im Auftrag

For the President of the European Patent Office

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RESISTANCE AGAINST WILT INDUCING FUNGI

FIELD OF THE INVENTION

5 The present invention relates to resistance genes, DNA constructs, micro-organisms, plant cells and plants comprising said resistance genes. Furthermore the invention relates to genetically transformed plants which are resistant against wilt inducing fungi. In addition, the invention relates to probes, and primers for the identification of the resistance genes and
10 diagnostic kits comprising said probes and/or primers. Finally, the invention relates to polypeptides encoded by said resistance genes and the use of said polypeptides.

BACKGROUND OF THE INVENTION

15 Plant pathogens such as fungi are responsible for substantial losses of plants and plant products due to infection of the plant. Plant diseases, as a result of infection by plant pathogens, cause damage to the plants and/or plant products, reduce production and yield, limit the kind of plants that can grow in certain geographic areas and as a result cause severe (financial)
20 losses to the grower.

 Different means for control of the plant pathogens exist, such as mechanical cultivation of the soil, chemical treatment with pesticides, including fungicides and insecticides, or crop rotation. However, for certain plant pathogens, especially soil born fungi, these means of control are
25 insufficient to protect the plants from infection and resulting diseases. The only effective means of control involves plant host resistance (Russell, 1978, Plant Breeding for pest and disease resistance, Butterworths edit., 485 pp). The development of cultivars resistant to common plant pathogens is one of the major goals of plant breeders today, in order to reduce or ultimately
30 eliminate the extensive need for pesticides. The burden for the environment of the large amounts of pesticides sprayed on crops, trees etc. worldwide

each year becomes too severe. Moreover, governmental regulations in Western countries restrict the use or even forbid the use of certain pesticides. Therefore, the need for plants which are resistant to one or more of their pathogens, or which have a reduced susceptibility to their attackers becomes more and more pressing.

Plants have developed a complex defense mechanism against attack and infection by pathogens. In general, their defense system is twofold, at the one hand it comprises a general resistance which is effective against different pathogen species, and at the other hand, it consists of a strong resistance against specific pathogen species. This latter resistance is generally based on a hypersensitivity reaction (HR). Although the exact defense mechanisms of the plant have still to be elucidated, it is assumed that when a pathogen comes into contact with a host cell, an early event takes place that triggers a rapid response that impedes further growth of the pathogen and subsequent development of the disease. Frequently within the pathogen population genotypes exist which can overcome this HR-resistance, so called races. If a host is resistant to a specific pathogen race, but susceptible to another race, one then speaks of race-specific resistance. It is furthermore believed that such a defense system in plant-pathogen interactions is based on a gene-for-gene relationship (Flor, 1956, *Adv.Gen.* 8, 29-54). In the gene-for-gene model it is postulated that for each gene conferring resistance to the host, there is a corresponding gene in the pathogen that confers avirulence, and vice versa. Very recently, evidence on molecular level for the gene-for-gene concept has been found with the cloning of a few plant resistance genes. The resistance gene of a plant encodes for a product, a receptor molecule, that can recognize a product of the pathogen, an elicitor, encoded by a avirulence gene. If the receptor interacts with the elicitor molecule a hypersensitive response is triggered, resulting into the destruction of the infected plant cells and surrounding cells, and so preventing the multiplication and spread of the pathogen within the plant. This postulated mechanism has recently been confirmed by the isolation of a few avirulence genes of the pathogen with the

corresponding resistance genes of the host plant. Examples of such resistance genes are: *RPS2* from *Arabidopsis* (resistance to *Pseudomonas syringae* expressing *avrRpt2*), *N* from tobacco (resistance to tobacco mosaic virus), *Cf-9* from tomato (resistance to the leaf fungal pathogen *Cladosporium fulvum* carrying *avr9*) and *L⁶* from flax (resistance to the corresponding leaf rust fungal race) (Dangl, 1995, Cell **80**, 363-366).

As stipulated before, the development of resistant plants is one of the important objectives of current plant breeding programs. Plant genotypes susceptible for particular pathogens are crossed with resistant plant genotypes in order to introduce the resistant phenotype into the breeding line. However, the breeding of resistance genes is restricted due to several factors: (i) the limited occurrence of (known) resistance genes in the available germplasm, (ii) incompatibility of crossing between different species and (iii) the limited availability of reproducible and reliable disease assays for certain pathogens, said assays being a prerequisite in selection breeding.

Amongst the pathogens causing serious damages to plants, one finds the group of soilborne cortical rots and vascular wilt inducing fungi, such as *Fusarium* and *Verticillium* (Toussoun, 1981, in: *Fusarium Diseases, Biology and Taxonomy*, Nelson, Toussoun & Cook edit., Penn. State Univ. Press, 457 pp.). Said wilt inducing fungi infect the plants through the roots via direct penetration or via wounds after which the xylem vascular tissue of the plant is colonized and symptoms of infection with said fungi are wilting, browning and dying of leaves followed by plant death. Entire plants or plant parts above the point of vascular invasion of the pathogen may die within a period of some weeks after infection. The fungi usually spread internally through the xylem vessels as mycelium or conidia until the entire plant is killed. Because of the fact that those fungi are able to survive in the soil saprophytically, they become established forever once they are introduced in the field. They are distributed more or less worldwide causing tremendous losses on most species of vegetables and flowers, field crops, fruit trees, etc. Because those

fungi are so widespread and so persistent in soils the only effective way of controlling said wilt inducing fungi is using resistant plant genotypes.

Most *Fusarium* species belong to the family of imperfect fungi. This class of fungi is characterized by the fact that only a vegetative stage of the fungus is known. The generative stage of those fungi has not been discovered yet. Due to the overall classification or taxonomy of fungi upon their morphological characteristics of the generative phase, one should bear in mind that fungi belonging to the class of imperfect fungi can be classified into another class once their generative stage is discovered and, subsequently, a change of classification and name can follow (Gerlach, 1981, in: *Fusarium, Diseases, Biology and Taxonomy*, Nelson, Toussoun & Cook edit., Penn. State Univ. Press, p. 413-426). Moreover, it has been observed that some *Fusarium* species can "mutate" into another species depending on the plant infected and/or the environment (Bolton & Davidson, 1972, *Can. J. Plant Sci*, **52**, 189-196). Up to now most of the wilt inducing *Fusarium* belong to the species *Fusarium oxysporum*. Different plant species are attacked by different races or isolates of *Fusarium* (Armstrong & Armstrong, 1981, in: *Fusarium, Diseases, Biology and Taxonomy*, Nelson, Toussoun & Cook edit., Penn. State Univ. Press, p. 391-399). However, some *Fusarium* isolates can infect different plant species. Known *Fusarium* isolates are for example: *Fusarium oxysporum* f.sp. *lycopersici* (tomato), *F. oxysporum* f.sp. *melonis* (melon), *F. oxysporum* f.sp. *batatas* (sweet potato, tobacco), *F. oxysporum* f.sp. *cepae* (onion), *F. oxysporum* f.sp. *conglutinans* (cabbage, radish), *F. oxysporum* f.sp. *cubense* (banana), *F. oxysporum* f.sp. *vasinfectum* (cotton, alfalfa, soybean, tobacco) *F. oxysporum* f.sp. *dianthii* (carnation), *F. oxysporum* f.sp. *chrysanthemi* (chrysanthemum), *F. oxysporum* f.sp. *tuberosi* (potato), *F. oxysporum* f.sp. *cyclaminis* (cyclamen).

In the light of the present invention it should be recognized that the name of the wilt inducing fungi can change in the future, but this will not effect the scope of the invention.

The isolation of plant genes without knowing their gene products is like looking for a needle in a haystack, because of the enormous genome sizes of plant species: e.g. tomato has a genome size of 1000 Mb (10^9 base pairs of nuclear DNA), maize has a genome size of 3000 Mb and wheat has even more than 16×10^9 base pairs. Searching for a specific gene among these billions of base pairs is only feasible when (i) there are enough molecular markers tightly linked to the gene of interest and (ii) there is good genetic material available (Tanksley *et al.*, 1995, Trends in Genetics, **11**, p. 63-68).

SUMMARY OF THE INVENTION

The present invention relates to a DNA sequence comprising the *I-2* resistance gene which when present and expressed in a plant is capable of conferring said plant resistant against wilt inducing fungi. Furthermore, the invention relates to the *I-2* resistance gene of which the DNA sequence is disclosed herein. The invention also relates to a gene product encoded by the *I-2* resistance gene which is capable of triggering a hypersensitive response in the plant when it comes into contact with a gene product encoded by a corresponding avirulence gene of the plant pathogen. In addition the present invention relates to DNA constructs, cosmids, vectors, bacterial strains, yeast cells and plant cells comprising the *I-2* resistance gene. In another aspect, the present invention relates to a genetically transformed plant, which is resistant to a wilt inducing fungus, said fungus being capable of infecting the untransformed plant. Furthermore, the invention relates to resistance genes which are homologous to the *I-2* resistance gene, and which, when present in a plant, are able of conferring said plant resistant to infection by pathogens.

Finally, the invention relates to oligonucleotides corresponding to the sequence of the *I-2* resistance gene or part thereof, and detection kits comprising said oligonucleotides.

DESCRIPTION OF THE FIGURES

Figure 1 shows a schematic representation of YAC 1/546, with a size of 750 kb, and the position of the *Bss*HII, *Rsa*I, *Sfi*I and *Sgr*A1 restriction sites (indicated by small lines). The hatched bar represents the 255 kb *Sgr*A1 fragment comprising the *I-2* resistance gene. The most lower line represents the size bar (in kb). The circle/arrowhead combination represents the left arm of pYAC4, direction of the centromer.

Figure 2 shows a schematic drawing of the binary cosmid vector pJJ04541 which is used to construct a cosmid library of YAC 1/546. Plasmid pRK290 (20 kb large)(Ditta *et al*, 1980, Proc. Natl. Acad. Sci. USA, **77**, 7347-7351) was used as starting vector. "Tet" refers to the gene conferring resistance to tetracyclin. "LB" signifies T-DNA left border repeat sequence, and "RB" signifies the right border repeat. The cauliflower mosaic virus 35S promoter sequence is indicated by "p35S", and "ocs3" indicates the octopine synthase 3' end. "NPT" indicates neomycin phosphotransferase, and "cos" refers to the bacteriophage lambda cos site enabling *in vitro* packaging. "pDBS" indicates the polylinker of pBluescript (Stratagene, La Jolla, CA, USA).

Figure 3 shows part of a 4,5% denaturing polyacrylamide gel with DNA fingerprints of 24 cosmids using Restriction Fragment Amplification with the enzyme combination *Eco*RI/*Mse*I. The templates used are depicted in the right part of the figure.

Figure 4 shows a schematic representation of the 255 kb *Sgr*A1 fragment with the position of the *Mlu*I and *Sa*I restriction sites (indicated with small lines) and the position of the 18 AFLP markers EM01 to EM18 (indicated with arrows). The cosmid contig of the DNA segment flanked by markers 18 and 12 is indicated with horizontal lines. The cosmids marked with an asterisk are used in the complementation analysis. The upper line represents the size bar (in kb) and the sizes of the *Mlu*I and *Sa*I restriction fragments are indicated.

Figure 5 shows a schematic representation of the overlapping cosmids A52 and B22 and partly of A55 and CC16 (the open arrow head indicates that the cosmid is continued). The position of the various restriction sites is indicated with small lines. The position of the AFLP markers EM05, EM14 and EM06 is indicated with an arrow. The DNA segment of which the nucleotide sequence was determined is indicated with a line with a bidirectional arrow.

Figure 6 shows the nucleotide sequence of a DNA segment of almost the complete overlap between cosmids A52, B22 and A55, and the deduced amino acid sequence of the *I*-2 resistance gene. The initiation codon (ATG position 1798-1800) is underlined and the termination codon (TAA position 5536-5538) is double underlined.

The position of the AFLP marker EM06 is from nucleotide position 3470 (5'-AATTCAGA-3') to nucleotide position 3565 (5'-**AGATTA**-5').

DETAILED DESCRIPTION OF THE INVENTION

In the description and examples that follow, a number of terms are used herein. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided:

- nucleic acid: a double-stranded DNA molecule;
- oligonucleotide: a short single-stranded DNA molecule;
- primers: in general, the term primer refers to a single-stranded DNA molecule which can prime the synthesis of DNA;
- nucleic acid hybridization: a method for detecting related DNA sequences by hybridization of single-stranded DNA on supports such as nylon membrane or nitrocellulose filter papers. Nucleic acid molecules that have complementary base sequences will reform the double-stranded structure if mixed in solution under the proper conditions. The double-stranded structure will be formed between two complementary single-stranded

nucleic acids even if one is immobilized on a support. In a Southern hybridization procedure, the latter situation occurs;

- hybridization probe: to detect a particular DNA sequence in the Southern hybridization procedure, a labelled DNA molecule or hybridization probe is reacted to the fractionated DNA bound to a support such as nylon membrane or nitrocellulose filter paper. The areas on the filter that carry DNA sequences complementary to the labelled DNA probe become labelled themselves as a consequence of the reannealing reaction. The areas of the filter that exhibit such labelling can then be detected according to the type of label used. The hybridization probe is generally produced by molecular cloning of a specific DNA sequence or by synthesizing a synthetic oligonucleotide;
- homologous sequence: a sequence which can hybridize under stringent conditions to a particular sequence, and/or a DNA sequence coding for a polypeptide which has the same properties as the polypeptide encoded by the particular DNA sequence, and/or a DNA sequence coding for a polypeptide having the same amino acid sequence as the polypeptide encoded by the particular DNA sequence and/or an amino acid sequence in which some amino acid residues have been changed with respect to the amino acid sequence of the particular polypeptide without effect on the properties of said polypeptide;
- promoter: a transcription regulation region upstream from the coding sequence containing the regulatory sequences required for the transcription of the adjacent coding sequence and includes the 5' non-translated region or so called leader sequence of mRNA;
- terminator: a region downstream of the coding sequence which directs the termination of the transcription, also called the 3' non-translated region, which includes the poly-adenylation signal;
- resistance gene: a nucleic acid having a coding sequence as depicted in Figure 6 or any corresponding or homologous coding sequence;

- stringent conditions refer to the hybridization conditions which allow an acid nucleic sequence to hybridize selectively to the I-2 resistance gene in its genomic environment, substantially to the exclusion of hybridization with other DNA sequences of said genomic environment.
- 5 – Fusarium 2: *Fusarium oxysporum* f.sp. *lycopersici* race 2 or any other genotype which is not able to infect a host having a resistance gene according to the invention;
- resistance gene product: a polypeptide having an amino acid sequence as depicted in Figure 6, or part thereof, or any homologous amino acid
10 sequence;
- R₀ plant: primary regenerant from a transformation experiment, also denoted as transformed plant or transgenic plant;
- R₁ line: the selfed progeny of a R₀ plant.

In the present invention we have been able to identify and isolate the
15 *Immunity-2 (I-2)* resistance gene. The gene was cloned from a tomato genotype which is resistant to *Fusarium oxysporum* f.sp. *lycopersici* race 2. The isolated I-2 resistance gene according to the invention can be transferred to a susceptible host plant using *Agrobacterium* mediated transformation or any other known transformation method, and is able to confer the host plant
20 resistant against Fusarium 2. The host plant can be tomato or any other genotype that is infected by Fusarium 2.

The present invention provides also the nucleic acid sequence of the I-2 resistance gene which is depicted in Figure 6.

With the I-2 resistance gene according to the invention, one has an
25 effective means for control against wilt inducing fungi, since the gene can be used for transforming susceptible plant genotypes thereby producing genetically transformed plants having a reduced susceptibility or being preferably resistant to infection by wilt inducing fungi. In a preferred embodiment the I-2 resistance gene comprises the coding sequence
30 preceded by a promoter region and followed by a terminator region. The promoter region should be functional in plant cells and, preferably,

corresponds to the native promoter region of the *I*-2 resistance gene. However, it should be recognized that any heterologous promoter region can be used in conjunction with the coding sequences, as long as it is functional in plant cells. Preferably, a constitutive promoter is used, such as the CaMV 35 S promoter or T-DNA promoters, all well known to the person skilled in the art. Furthermore, a suitable terminator region should be functional in plant cells all well known to the person skilled in the art.

In addition the invention relates to the *I*-2 resistance gene product which is encoded by the *I*-2 resistance gene according to the invention and which has an amino acid sequence which is homologous to the deduced amino acid sequence or part thereof as listed in Figure 6. The *I*-2 resistance gene product can be used for the identification and/or isolation of the corresponding gene product encoded by an avirulence gene of the pathogen. The relationship between the *I*-2 resistance gene product, which is acting like a receptor molecule, and the gene product of the pathogen, which is acting like an elicitor molecule, is characterized by the occurrence of a defense mechanism reaction in the plant. Furthermore the *I*-2 resistance gene product can be used for raising antibodies against it, which antibodies can be used for the detection of the presence of the *I*-2 resistance gene product.

In another aspect of the invention, the *I*-2 resistance gene can be used for the design of oligonucleotides which are complementary to one strand of the DNA sequence as described in Figure 6, or part thereof, which can be used as hybridization probes, being accordingly labelled to allow detection, for the screening of genomic DNA or cDNA libraries for homologous genes. Homologous sequences which can hybridize to the probe, which encode for a gene product that is able to confer resistance to a plant against a fungus which normally infects said plant, or both are comprised within the scope of the present invention.

In another aspect of the invention oligonucleotides are designed based on the *I*-2 resistance gene sequence, such that they can be used as hybridization probes in Southern analysis. These probes can be used as

molecular markers to distinguish plant genotypes having the resistance gene and plant genotypes lacking the resistance gene. Such a probe can be used as an additional tool in selection breeding. In a preferred embodiment of the invention, oligonucleotides are designed on the *I-2* resistance gene sequence, such that they can be used as primers in an amplification reaction, such as polymerase chain reaction (PCR), whereby the formation of an amplification product indicates the presence of the *I-2* resistance gene in a certain plant genotype. In a particular embodiment of the invention said primers direct the amplification of polymorphic fragments, so called molecular markers, which are closely linked to the *I-2* resistance gene. The invention also relates to diagnostic kits, comprising oligonucleotides according to the invention, for the detection of the presence or absence of the *I-2* resistance gene within a genotype under study. Such a diagnostic kit circumvents the use of a laborious disease assay to screen for genotypes having the resistance gene or not.

Furthermore the invention relates to DNA constructs (A) comprising a DNA sequence corresponding to the coding sequence of the *I-2* resistance gene and regulatory sequences functional in plant cells. Said regulatory sequences are either homologous or heterologous to the coding sequences of the *I-2* resistance gene. The invention relates also to DNA constructs (B) comprising the regulatory sequences, and more preferably the promoter region of the *I-2* resistance gene in conjunction with a structural gene sequence heterologous to said regulatory sequences.

The invention relates also to a DNA vector comprising a DNA construct (A) and/or (B). Suitable vectors can be cloning vectors, transformation vectors, expression vectors, etc., which are well known to the skilled person in the art. Furthermore, cells harbouring a vector comprising a DNA sequence corresponding to the sequence as described in Figure 6 or part thereof, DNA constructs (A) or DNA constructs (B), are within the scope of the invention.

In one preferred embodiment of the invention, a genetically transformed plant is obtained by introducing the *I-2* resistance gene within the genome of said plant, having a susceptible genotype to *Fusarium* 2, using standard transformation techniques, wherein said genetically transformed plant is resistant to *Fusarium* 2.

Surprisingly, we have found that the *I-2* resistance gene, is functional in heterologous systems, such as melon, tobacco, *Arabidopsis*, potato species, and is capable of conferring these plant species resistant against one or more wilt inducing fungi.

The DNA sequence comprising the *I-2* resistance gene as provided in the present invention has numerous applications of which some are described herein but which are not limiting the scope of the invention.

The present invention will be further described in detail in view of the isolation of the *I-2* resistance gene present in tomato lines which are resistant against *Fusarium oxysporum* f.sp. *lycopersici* race 2. For the isolation of the *I-2* resistance gene we have used a map-based cloning (positional cloning) strategy, comprising the following steps:

- (1) identification of molecular markers linked to the *I-2* resistance gene,
- (2) genetic mapping of the *I-2* locus using morphological markers,
- (3) construction of a high molecular weight genomic YAC library,
- (4) physical mapping of the molecular markers on the YAC clones and YAC contig building,
- (5) construction of a cosmid library of the YAC clone harbouring the linked molecular markers,
- (6) physical fine mapping and cosmid contig building,
- (7) transformation of susceptible plants with the cosmids forming the contig,
- (8) complementation analysis.

For the identification of molecular markers, we have used the selective restriction fragment amplification technology, hereinafter denoted as AFLP™ technology, which randomly amplifies a subset of DNA fragments out of a

complex mixture of many DNA fragments and said amplified fragments generate fingerprints that can be analyzed

5 In general, total DNA of different genotypes of the same plant species are subjected to the AFLP technology and the different AFLP fingerprints obtained from the different genotypes are compared. Fragments that are present in one genotype and absent in another genotype are polymorphic fragments and are denoted as AFLP markers.

10 The selectivity in AFLP reactions is obtained by using randomly chosen selective nucleotides at the 3' end of the PCR primers immediately adjacent to the nucleotides of the restriction enzyme site. In an AFLP screening the DNA to be studied is subjected to different primer combinations. The total amount of different primers that can be used is determined by the number of selective nucleotides that are added to the 3' end (4 primers with 1 selective nucleotides, 16 primers with 2 selective
15 nucleotides, 64 primers with 3 selective nucleotides). If two different restriction enzymes are used than there are twice the amount of primers. Those primers can be used in different combination. If all possible combinations are used in an AFLP screening, than all the fragments present should have been amplified with one of the primer combinations (Zabeau and
20 Vos, EP 0534858).

For the identification of AFLP markers linked to the *I-2* resistance gene different tomato lines were subjected to an AFLP screening. The tomato lines were pooled into different pools: on the one hand pools of tomato lines being resistant against *Fusarium 2* and on the other hand pools of tomato lines
25 being susceptible to *Fusarium 2*.

The pools were subjected to an AFLP screening using the *EcoRI/MseI* enzyme combination.

The following primers are used for the AFLP screening:

EcoRI-primers: 5'-GACTGCGTACCAATTCNNN-3'
30 *MseI*-primers: 5'-GATGAGTCCTGAGTAANNN-3'

The N's indicate the variable selective nucleotides. In the AFLP screening all 64 possible primers were used for both the *EcoRI*- and *MseI*-primer giving a total of $64 \times 64 = 4096$ primer combinations. The objective of the screening was to identify AFLP markers linked to the *I-2* resistance gene, i.e. present in the fingerprints of the resistant pools, and absent in the fingerprints of susceptible pools. In the analysis of all the AFLP fingerprints a total of 18 AFLP markers were identified which were present in the resistant pools and absent in the sensitive pools: these markers are referred to as candidate *I-2* linked AFLP markers.

The presence of these candidate *I-2* linked AFLP markers were confirmed on the individual tomato lines. All markers were present in the resistant lines and absent in the susceptible lines.

However, the position of the AFLP markers with respect to the *I-2* resistance gene and the distance between the *I-2* resistance gene and the respective markers has still to be determined. For that purpose a genetic map of the *I-2* locus was made by making genetic crosses between *Fusarium* 2 resistant tomato lines and susceptible tomato lines having morphological markers, followed by a screening for recombinants in the segregating F2 populations and screening of the F2 recombinants with the AFLP markers. The results indicated that the *I-2* locus is flanked by marker EM18 at one end of the DNA segment comprising the *I-2* resistance gene and markers EM03, EM12 and EM16 at the other end. All the other AFLP markers co-segregated with the *I-2* resistance gene.

Next, the AFLP markers were screened on a high molecular weight genomic library. The cloning of very large segments of DNA as large artificial chromosomes in yeast has become an essential step in isolating genes via positional cloning. The cloning capacity of the YAC vector allows the isolation of DNA fragments up to one million base pairs in length. The tomato line *Lycopersicon esculentum* E22, homozygous for the *I-2* locus, was used as source DNA to construct a YAC library. We obtained a YAC library containing 3840 clones with an average insert size of 520 Kb, representing

approximately 2.2 genome equivalents of the tomato genome. One positive clone was obtained after an AFLP screening with the *I*-2 linked AFLP markers, and all markers were present on this individual YAC clone, designated as YAC 1/546. The size of this YAC clone is determined to be 750 kb.

Further analysis has determined that all of the AFLP markers were located on a *Sgr*AI fragment, at a distance of 255 kb of the left arm of the YAC until the first *Sgr*AI site. A schematic representation of the physical map of the left arm of YAC 1/546, containing the *I*-2 locus, including the location of the 18 AFLP markers, is depicted in Figure 4. The exact location of the AFLP markers can be determined on the basis of mapping cosmids on the physical map.

The size of an insert in YAC 1/546 is still too large for direct localization of the *I*-2 gene. Such large inserts cannot be transformed into plant cells directly. Therefore, a cosmid library was constructed of the yeast strain containing YAC 1/546 using cosmid vectors which are suitable for *Agrobacterium* mediated transformation. The size of this binary cosmid vector amounts 29 kb and is shown schematically in Figure 2. The cloning capacity of this binary cosmid vector, using phage lambda packaging extract is within the range of 9 to 24 kb. A bank of approximately 250,000 cosmid clones was obtained from size fractionated yeast DNA. The cosmid bank was screened by colony hybridization using the labelled *Sgr*AI fragment as probe. Of about 10,000 colonies approximately 150 positive cosmid clones were identified.

In the following step, the position of the AFLP markers on the 255 kb *Sgr*AI fragment was determined on the basis of a cosmid contig. The positive cosmid clones were screened with the 18 AFLP markers and their position was determined. A schematic outline of the cosmid contig and the physical fine mapping of the 18 AFLP markers is depicted in Figure 4.

The final step in the identification of the *I*-2 resistance gene via positional cloning is the complementation of the corresponding susceptible phenotype. The cosmid clones were introduced in *Agrobacterium*

tumefaciens through conjugative transfer in a tri-parental mating. The presence of the cosmid in the *A. tumefaciens* strains was determined comparing various restriction enzyme patterns as well as DNA fingerprints from the *A. tumefaciens* strains with the *E. coli* strain containing the cosmid. Only those *A. tumefaciens* cultures harbouring a cosmid with the same DNA pattern as the corresponding *E. coli* culture were used to transform a susceptible tomato line.

A susceptible tomato line was transformed with several cosmids forming the cosmid contig using standard transformation methods.

The primary regenerants (R_0 plants) of the transformation experiments were grown in the greenhouse for seed set to obtain R_1 lines. These were tested for disease symptoms in order to identify cosmids with the resistance gene. The disease assay is performed on seedlings. Their roots are immersed in a conidial suspension of *Fusarium oxysporum* f.sp. *lycopersici* race 2 and disease symptoms are scored three to four weeks after inoculation. Plants are scored resistant when they are healthy without browning of the stem tissue. Plants being dead or having yellow wilting leaves and having severe browning of the stem tissue are scored susceptible. The observations of the disease assay revealed that 3 cosmids were able to complement the susceptible phenotype, thereby providing definitive evidence that a functional *I-2* resistance gene is located on each of these 3 cosmids.

To demonstrate that the resistant phenotype of the transgenic R_0 plants, which were transformed with the overlapping cosmids A52, B22 and A55, is determined by the genomic insert present in the various cosmids, the presence of the corresponding AFLP markers was investigated. Selective restriction fragment amplification was performed with the primer combinations identifying the markers EM14 and EM06 for the R_0 plants transformed with cosmids A52 and B22 and with the primer combinations identifying the markers EM06 and EM04 for the R_0 plants transformed with cosmid A55. The DNA fingerprints obtained showed in both cases and for both markers the presence of the markers in the resistant plants and the absence of the

markers in the susceptible plants indicating that the three identified overlapping cosmids A52, B22 and A55 contain the *I-2* resistance gene.

Finally, the inserts in cosmids A52, B22 and A55 were further characterized, and the minimal DNA segment comprising the *I-2* resistance gene, defined by the left end of cosmid A55 and the right end of cosmid B22, was sequenced. Sequencing analysis revealed a large open reading frame of 3798 nucleotides. The DNA sequence is listed in Figure 6.

Cosmid B22 was used for the transformation of susceptible genotypes of melon, tobacco as well as Arabidopsis according to general known transformation methods. The R_0 plants were grown in the greenhouse for seed set to obtain R_1 lines. These were tested for disease symptoms in order to identify the functionality of the *I-2* resistance gene. The disease assay was performed on seedlings as described herein. Cosmid B22 was also used for the transformation of a susceptible genotype of potato. Vegetatively propagated transformed plants were obtained and were subjected to the disease assay. The observations of the disease assay on the transformed plants revealed the complementation of the susceptible phenotype.

For the identification and isolation of homologous sequence falling within the scope of the present invention, genomic and cDNA libraries were screened with the coding sequence of the *I-2* resistance gene as a probe under stringent hybridization conditions. Positive clones were isolated and were used for complementation analysis.

Plasmid pKGI2-B22 has been deposited on July 14, 1995 at Centraalbureau voor Schimmelcultures at Baarn, The Netherlands, under deposit number CBS 546.95.

The following examples will provide a further illustration of the present invention which is nevertheless not limited to these examples.

EXAMPLES

EXAMPLE 1: DISEASE ASSAY

Fusarium oxysporum forma specialis *lycopersici* race 2 was maintained on Czapek Dox Agar (Difco Laboratories, Detroit, MI, USA). Conidial suspensions were obtained by culturing the fungus in Czapek Dox Broth (Difco Laboratories, Detroit, MI, USA) on a reciprocal shaker for 4 to 7 days at 25° Celsius. The conidia were separated from mycelium fragments by filtration through a stainless steel filter with a pore size of 50 mm. The suspensions were adjusted to a concentration of 2×10^6 conidia per ml by diluting with water.

Seeds of tomato were germinated in soil in the greenhouse at 25° Celsius. Ten to 14 days-old seedlings were used for inoculation with the fungus. The seedlings were carefully pulled out of the soil and the roots were dipped in water for removing most of the adhering soil. Subsequently, the roots were immersed in the conidial suspension for two minutes and the plants were repotted in soil. The plantlets were grown in the greenhouse at a temperature of 25° C at daytime (16 hours) and 22° C at night (8 hours). After three to four weeks the plants were scored for disease symptoms.

The plants were evaluated as follows: Resistant plants resemble non-inoculated plants; they are large and without browning of stem tissue. Susceptible plants are dead or show typical symptoms: small plants with yellow, wilting leaves and severe browning of stem tissue.

EXAMPLE 2: IDENTIFICATION OF AFLP MARKERS LINKED TO A DNA SEGMENT COMPRISING THE *I-2* RESISTANCE GENE

Tomato lines (*Lycopersicon esculentum*)

A total of 10 *F. oxysporum* f.sp. *lycopersici* race 2 resistant and 10 *F. oxysporum* f.sp. *lycopersici* race 2 susceptible tomato lines were used, and are depicted below:

	1.	DR9	resistant	De Ruiter Zonen C.V., Bleiswijk, The Netherlands (hereinafter "De Ruiter")
	2.	RZ5	resistant	Rijk Zwaan Zaadteelt en Zaadhandel B.V., De Lier, The Netherlands (hereinafter "Rijk Zwaan")
5	3.	E22	resistant	Enza Zaden, de Enkhuizer Zaadhandel B.V., Enkhuizen, The Netherlands (hereinafter "Enza Zaden")
	4.	E16	resistant	Enza Zaden
10	5.	DR4	resistant	De Ruiter
	6.	RZ7	resistant	Rijk Zwaan
	7.	E3	resistant	Enza Zaden
	8.	E7	resistant	Enza Zaden
	9.	RZ4	resistant	Rijk Zwaan
15	10.	DR12	resistant	De Ruiter
	11.	GCR210	susceptible	Institute of Horticultural Research, Littlehampton, Great Britain
	12.	GCR508	susceptible	Institute of Horticultural Research, Littlehampton, Great Britain
20	13.	52201	susceptible	Rijk Zwaan
	14.	DR5	susceptible	De Ruiter
	15.	E12	susceptible	Enza Zaden
	16.	E1	susceptible	Enza Zaden
	17.	RZ8	susceptible	Rijk Zwaan
25	18.	E6	susceptible	Enza Zaden
	19.	RZ10	susceptible	Rijk Zwaan
	20.	DR11	susceptible	De Ruiter

Isolation and modification of the DNA

Total tomato DNA from the 20 lines described above was isolated from young leaves as described by Bernatzki and Tanksley (1986, Theor. Appl. Genet. 72, 314-321). The typical yield was 50 - 100 mg DNA per gram of fresh leaf material. Template DNA for AFLP analysis with the enzyme combination *EcoRI-MseI* was prepared as described by Zabeau and Vos (European Patent Application, EP 0534858), and is described briefly below:

0.5 mg of tomato DNA was incubated for 1 hour at 37 °C with 5 units *EcoRI* and 5 units *MseI* in 40ml 10 mM Tris.HAc pH 7.5, 10 mM MgAc, 50 mM KAc, 5 mM DTT, 50 ng/ml BSA. Next 10 ml of a solution containing 5 pMol *EcoRI*-adapters, 50 pMol *MseI*-adapters, 1 unit T4 DNA-ligase, 1 mM ATP in 10 mM Tris.HAc pH 7.5, 10 mM MgAc, 50 mM KAc, 5 mM DTT, 50 ng/ml BSA was added, and the incubation was continued for 3 hours at 37°C. The adapters are depicted below:

The structure of the *EcoRI*-adapter was:

5'-CTCGTAGACTGCGTACC
CATCTGACGCATGGTTAA-5'

The structure of the *MseI*-adapter was:

5'-GACGATGAGTCCTGAG
TACTCAGGACTCAT-5'

Adapters were prepared by adding equimolar amounts of both strands; adapters were not phosphorylated. After ligation, the reaction mixture was diluted to 500 ml with 10 mM Tris.HCl, 0.1 mM EDTA pH 8.0, and stored at -20°C. The diluted reaction mixture is further referred to as template DNA.

AFLP reactions

The primers used for the AFLP screening are depicted below:

EcoRI-primers: 5'-GACTGCGTACCAATTCNNN-3'

MseI-primers: 5'-GATGAGTCCTGAGTAANNN-3'

The N's in the primers indicate that this part of the primers was variable. In the AFLP screening all 64 possible primers were used for both

the *EcoRI*- and *MseI*-primer. This gave a total of 64 x 64 combinations of *EcoRI*- and *MseI*-primers, is 4096 primer combinations. All 4096 primer combinations were used in the AFLP screening for *I*-2 linked AFLP markers. The AFLP reactions were performed in the following way:

AFLP reactions employed a radio-actively labelled *EcoRI*-primer and a non-labelled *MseI*-primer. The *EcoRI*-primers were end-labelled using (g-³³P)ATP and T4 polynucleotide kinase. The labelling reactions were performed in 50 ml 25 mM Tris.HCl pH 7.5, 10 mM MgCl₂, 5 mM DTT, 0.5 mM spermidine.3HCl using 500 ng oligonucleotide primer, 100 mCi (g-³³P)ATP and 10 units T4 polynucleotide kinase. For AFLP analysis 20 ml reaction mixture were prepared containing 5 ng labelled *EcoRI*-primer (0.5 ml from the labelling reaction mixture), 30 ng *MseI*-primer, 5 ml template-DNA, 0.4 units Taq-polymerase, 10 mM Tris.HCl pH 8.3, 1.5 mM MgCl₂, 50 mM KCl, 0.2 mM of all 4 dNTPs. AFLP reactions were performed using the following cycle profile: a 30 seconds DNA denaturation step at 94 °C, a 30 seconds annealing step (see below), and a 1 minute extension step at 72 °C. The annealing temperature in the first cycle was 65 °C, was subsequently reduced each cycle by 0.7 °C for the next 12 cycles, and was continued at 56 °C for the remaining 23 cycles. All amplification reactions were performed in a PE-9600 thermocycler (Perkin Elmer Corp., Norwalk, CT, USA).

Gel analysis of AFLP reaction products

After amplification, reaction products were mixed with an equal volume (20 ml) of formamide dye (98% formamide, 10 mM EDTA pH 8.0, and bromo phenol blue and xylene cyanol as tracking dyes). The resulting mixtures were heated for 3 minutes at 90°C, and then quickly cooled on ice. 2 ml of each sample was loaded on a 5% denaturing (sequencing) polyacrylamide gel (Maxam and Gilbert, 1980, Methods in Enzymology 65, 499-560). The gel matrix was prepared using 5% acrylamide, 0.25% methylene bisacryl, 7.5 M urea in 50 mM Tris/50 mM Boric acid/1 mM EDTA. To 100 ml of gel solution 500 ml of 10% APS and 100 ml TEMED was added and gels were cast using

a SequiGen 38 x 50 cm gel apparatus (Biorad Laboratories Inc., Hercules, CA, USA). Sharktooth combs were used to give 97 lanes on the SequiGen gel units. 100 mM Tris/100 mM Boric acid/2 mM EDTA was used as running buffer. Electrophoresis was performed at constant power, 110 Watts, for approximately 2 hours. After electrophoresis, gels were fixed for 30 minutes in 10% acetic acid dried on the glass plates and exposed to Fuji phospho image screens for 16 hrs. Fingerprint patterns were visualized using a Fuji BAS-2000 phospho image analysis system (Fuji Photo Film Company Ltd, Japan).

AFLP screening for linked markers

The template DNAs of the 20 tomato lines were pooled in the following way:

resistant pool 1:	tomato lines 1 - 5
resistant pool 2:	tomato lines 6 - 10
susceptible pool 3:	tomato lines 11 - 15
susceptible pool 4:	tomato lines 16 - 20

An AFLP screening was performed using all possible 4096 *EcoRI*-*MseI* primer combinations on the 4 pools. The aim was to identify AFLP markers present in both resistant pools, and absent in both sensitive pools. AFLP gels contained the AFLP fingerprints of 24 primer combinations of the 4 pools, giving a total of 171 gels. Additional gels were run to reanalyse unsuccessful AFLP reactions and to confirm candidate markers. A total of 18 AFLP markers were identified present in both resistant pools and absent in both susceptible pools: these markers were referred to as candidate *I*-2 linked markers.

Next AFLP reactions were performed to determine the presence of all 18 candidate markers on the 20 individual tomato lines. All markers appeared to be present in the 10 resistant lines and absent in the 10 susceptible lines. These 18 markers were named EM01 to EM18 and were used in further

studies to map the *I-2* Fusarium resistance gene. The primer combinations required to identify markers EM01 to EM18 are depicted in Table 1. In the column with the primer combinations, "EcoRI-" refers to the sequence 5'-GACTGCGTACCAATTC-3' and "MseI-" refers to the sequence 5'-GATGAGTCCTGAGTAA-3'. For example, marker EM06 can be identified using the *EcoRI*-primer having the following sequence: 5'-GACTGCGTACCAATTCAGA-3', and the *MseI*-primer having the following sequence: 5'-GATGAGTCCTGAGTAATCT-3'.

TABLE 1

marker	primer combination containing selective extensions (NNN)
EM01	<i>EcoRI</i> -AAA / <i>MseI</i> -AGG
EM02	<i>EcoRI</i> -CCA / <i>MseI</i> -TCA
EM03	<i>EcoRI</i> -CTC / <i>MseI</i> -GCT
EM04	<i>EcoRI</i> -GAG / <i>MseI</i> -GTC
EM05	<i>EcoRI</i> -TCT / <i>MseI</i> -AAG
EM06	<i>EcoRI</i> -AGA / <i>MseI</i> -TCT
EM07	<i>EcoRI</i> -CTT / <i>MseI</i> -AAG
EM08	<i>EcoRI</i> -CAA / <i>MseI</i> -GCT
EM09	<i>EcoRI</i> -GTC / <i>MseI</i> -GTC
EM10	<i>EcoRI</i> -TGT / <i>MseI</i> -AAT
EM11	<i>EcoRI</i> -TAG / <i>MseI</i> -AGC
EM12	<i>EcoRI</i> -TGC / <i>MseI</i> -AAG
EM13	<i>EcoRI</i> -TAA / <i>MseI</i> -ACC
EM14	<i>EcoRI</i> -TGC / <i>MseI</i> -AGA
EM15	<i>EcoRI</i> -CTT / <i>MseI</i> -ATG
EM16	<i>EcoRI</i> -CAT / <i>MseI</i> -AGT
EM17	<i>EcoRI</i> -CTC / <i>MseI</i> -AGC
EM18	<i>EcoRI</i> -CGG / <i>MseI</i> -CAC

EXAMPLE 3: GENETIC MAPPING OF THE TOMATO *I-2* LOCUS

Development of genetic material

Two *F. oxysporum* f.sp. *lycopersici* race 2 resistant tomato
 5 (*Lycopersicon esculentum*) lines have both been crossed with the susceptible
 tomato lines GCR210 and GCR508. Both resistant lines, DR9 and RZ5, are
 breeding lines from two seed companies, De Ruiter Zonen and Rijk Zwaan,
 respectively. The susceptible tomato line GCR210 is homozygous for the
 recessive morphological marker gene *a* (anthocyaninless). The susceptible
 10 line GCR508 is homozygous for the recessive morphological marker gene
sub (*subtilis*) (Stevens and Rick, 1986, in: The Tomato Crop, Atherton &
 Rudich edit., Chapman and Hall, p. 35-109). Both susceptible lines were
 obtained from the Institute of Horticultural Research (Littlehampton, United
 Kingdom).

15 The dominant *I-2* gene (conferring resistance to *F. oxysporum* f.sp.
lycopersici 2), and recessive genes *a* and *sub* have all been mapped to the
 long arm of chromosome 11 of tomato (Stevens and Rick, 1986, in: The
 Tomato Crop, Atherton & Rudich edit., Chapman and Hall, p. 35-109): *I-2* on
 position 85 of this chromosome, *a* on position 68 (17 centiMorgans (cM) from
 20 *I-2*), and *sub* on position 89 (4 cM from *I-2*).

The crosses made are depicted below:

Cross 1: DR9 (+ +, *I-2 I-2*) x GCR210 (*a a*, *i-2 i-2*)
 Cross 2: RZ5 (+ +, *I-2 I-2*) x GCR210 (*a a*, *i-2 i-2*)
 Cross 3: DR9 (*I-2 I-2*, + +) x GCR508 (*i-2 i-2*, *sub sub*)
 25 Cross 4: RZ5 (*I-2 I-2*, + +) x GCR508 (*i-2 i-2*, *sub sub*)

F_1 plants from all crosses were selfed for generating F_2 seeds. The
 resulting F_2 populations will segregate for resistance to *F. oxysporum* f.sp.
lycopersici 2 and for the morphological markers.

Selection of recombinants in the region containing *I-2*

3000 F₂ seeds from the crosses 1 and 2 with GCR210 (containing *a*) were germinated. After 10 to 14 days, the seedlings were divided in two groups: one with purple-coloured hypocotyls (wild type seedlings) and the other with green hypocotyls (seedlings homozygous *a*). 330 wild type seedlings and 565 anthocyaninless seedlings were inoculated with *F. oxysporum* f.sp. *lycopersici* race 2. After three to four weeks the plants were scored for resistance/susceptibility. The results are shown below:

phenotype	resistant	susceptible
wild type	278	52
anthocyaninless	169	396

The recombinants are susceptible wild type plants and resistant anthocyaninless plants.

1500 F₂ seeds from the crosses 3 and 4 with GCR508 (containing *sub*) were germinated. After 10 to 14 days, the seedlings were inoculated with *F. oxysporum* f.sp. *lycopersici* race 2. During the assay the plantlets were phenotypically scored for growth habit, normal or 'subtilis', and for resistance/susceptibility. The results are shown below:

phenotype	resistant	susceptible
wild type	913	38
subtilis	183	51

The recombinants are susceptible wild type plants and resistant 'subtilis' plants.

F₂ plants were grown in the greenhouse for seed set (by induced or spontaneous selfing). F₃ seeds were obtained from most of the resistant recombinant F₂ plants and from a few of the susceptible recombinants. These

F_3 lines were tested for resistance/ susceptibility in order to check the phenotype of the F_2 plants. Twenty to 30 seedlings of each F_3 line were inoculated with *F. oxysporum* f.sp. *lycopersici* 2 and evaluated as described in Example 1. The F_3 progenies of the resistant recombinants did segregate 3:1 for resistance, while those of the susceptible recombinants scored all susceptible.

Screening of AFLP markers in F_2 recombinants

An AFLP analysis with the 18 identified *I*-2 markers EM01 to EM18 has been performed on 187 resistant recombinant plants, 10 susceptible recombinant plants, and 39 control plants (12 resistant and 27 susceptible) as described in Example 2.

The following results were obtained:

- The markers EM01, EM02, EM04, EM05, EM06, EM07, EM08, EM09, EM10, EM11, EM13, EM14, EM15 and EM17 were present in all 199 resistant F_2 plants and absent in all 37 susceptible plants; these markers are closely linked to the *I*-2 gene.
- The markers EM03, EM12 and EM16 were present in all resistant plants and absent in the susceptible plants with the exception of one anthocyaninless plant.
- The marker EM18 is present in all resistant plants except for seven anthocyaninless plants, and absent in all susceptible plants.

From these data it could be concluded that the *I*-2 locus is flanked by marker EM18 at one end of the DNA segment comprising the *I*-2 resistance gene and on the other end by the markers EM03, EM12 and EM16. All of the remaining markers completely co-segregate with the *I*-2 resistance gene based on the analysis of recombinants of crosses as described above.

EXAMPLE 4: CONSTRUCTION AND SCREENING OF A TOMATO YAC-LIBRARY

Material

5 The tomato line *Lycopersicon esculentum* E22 (Enza Zaden) homozygous for the *I-2* locus, was used as source DNA to construct a YAC-library. Protoplasts were isolated from the leaves of *in vitro* shoots which were two to three weeks old as described by Van Daelen *et al.* (1989, Plant Mol. Biol. **12**, 341-352).

10 Viable protoplasts (concentration of 50 million protoplasts per ml) were collected and mixed with an equal volume of agarose (1%, Seaplaque, FMC BioProducts, Rockland, Maine, USA) to form a plug. The protoplasts embedded into the plugs were lysed with lysis mix (0.5 M EDTA, 1% N-Laurylsarcosinate and 1 mg/ml proteinase K, pH= 8.0). After lysis, the plugs were stored at 4 °C in storage buffer (fresh lysis mix) until used.
15 Approximately 3 million protoplasts per plug, to obtain about 4.5 mg of chromosomal DNA were used for further studies. Plasmid pYAC4 containing an unique *EcoRI* cloning site was used as cloning vector and the yeast strain AB1380 was used as a host (Burke *et al.*, 1987, Science **236**, 806-812).

20 YAC library construction

High molecular weight DNA isolation, partial digestion with *EcoRI* in the presence of *EcoRI* methylase, ligation of vector arms to genomic DNA, size selection by pulsed field gel electrophoresis and transformation of the yeast host was performed as described by Burke *et al.* (1987, Science **236**,
25 806-812) and Larin *et al.* (1991, Proc. Natl. Acad. Sci. USA **88**, 4123-4127).

All standard manipulations were carried out as described in Molecular cloning: a laboratory manual by Sambrook *et al.*, (1989, Cold Spring Harbor Laboratory Press).

30 3840 clones with a average insert size of 520 kb, which corresponds to 2.2 genome equivalents were finally obtained and the individual clones

were stored in 40 96-wells microtiter plates containing 75 ml YPD solution (1% yeast extract, 2% peptone and 2% dextrose).

Screening YAC library

5 To reduce the number of samples handled, the cells of one 96-well microtiter plate was pooled (a plate pool) and used for DNA isolation as described by Ross *et al.* (1991, Nucleic Acids Res., **19**, 6053). The 2.2 genome equivalent tomato YAC library consists of 40 96-wells microtiter wells and as a result DNA of the 40 plate pools were screened with the AFLP-
10 markers EM01, EM12 and EM18 (see Example 2) using the AFLP-protocol as described in Example 2. One positive plate pool out of the 40 was identified with all three AFLP-markers. Subsequently, a secondary screening of the 96 individual YAC clones was employed to find the correct address of the YAC or YACs. One individual YAC clone was identified, designated 1/546, and
15 subsequently analyzed with the remaining AFLP markers. As expected, all of identified markers EM01 to EM18 were present on this YAC-clone since the flanking markers and one co-segregating marker were used in the screening. The size of the YAC-clone was determined by Pulse-field gel electrophoretic (PFGE) analysis using contour-clamped homogeneous electric field (CHEF; Chu *et al.* 1986, Science, **235**, 1582-1585) and appeared to be 750 kb.
20

EXAMPLE 5: CONSTRUCTION OF A PHYSICAL MAP OF YAC 1/546 AND LOCATION OF THE AFLP MARKERS

25 YAC 1/546 was subjected to partial digestion with increasing concentration of the restriction enzymes *SgrA1*, *RsrII*, *SfiI* and *BssHII*. The samples were fractionated by PFGE, transferred to a Gene Screen Plus membrane (DuPont NEN, Boston, MA, USA) and assayed by hybridization using end-adjacent sequence probes according to the protocol for indirect end-label mapping as described by Burke *et al.* (1987, Science **236**, 806-
30 812).

In Figure 1 a schematic representation is given of the physical map of YAC 1/546.

To determine the position of the various AFLP markers on the physical map, the AFLP markers were used as hybridization probes on the partial digests of YAC 1/546. Therefore, the AFLP-marker fragment was excised from the dried gel and eluted by means of diffusion in a buffer containing 0.5 M ammonium acetate, 10 mM magnesium acetate, 1 mM EDTA (pH=8.0), 0.1% SDS, re-amplified with the PCR primers used in the AFLP reaction and labelled with ^{32}P according to the random primer method of Feinberg and Vogelstein (1983, Anal. Biochem. **132**, 6-10).

It appeared that all of the AFLP-markers were located on a *SgrA1* fragment, at a distance of 255 kb of the left arm of the YAC until the first *SgrA1* site.

15 **EXAMPLE 6: CONSTRUCTION OF A COSMID LIBRARY OF YAC 1/546**

Material

The binary cosmid vector pJJ04541 is a derivative of pJJ1881 (Jones *et al.*, 1992, Transgenic Research **1**, 285-297) and is based on plasmid pRK290 containing the tetracyclin resistance gene for selection in *Escherichia coli* and *Agrobacterium tumefaciens*. Into the unique *EcoRI* site of pRK290, T-DNA carrying sequences (LB; left border repeat, RB signifies the right border repeat) that flank:

- the cos site of bacteriophage lambda
- the neomycin phosphotransferase gene (Beck *et al.*, 1982, Gene **19**, 327-336) whose expression is driven by the cauliflower mosaic virus 35S promoter sequence (Odell *et al.*, 1984, Mol. Gen. Genet. **223**, 369-378), and
- the pBluescript (Stratagene, La Jolla, CA, USA) polylinker sequence.

The size of pJJ04541 amounts 29 kb and is shown schematically in Figure 2. The cloning capacity of this binary cosmid vector, using phage lambda packaging extracts is within the range of 9 to 24 kb.

Library construction

Total DNA of the *Saccharomyces cerevisiae* strain AB1380 containing YAC 1/546 was isolated using zymolyase to make protoplasts according to Green and Olsen (1990, Proc. Natl. Acad. Sci. USA **87**, 1213-1217).

An aliquot was analyzed on PFGE and appeared to have a size of ≈ 100 kb.

Approximately 15 mg of this DNA was partially digested with *Sau3A* generating molecules with an average size of 15-25 kb. Subsequently, this sample was centrifugated through a 10-35% sucrose gradient for 22 hours, 22.000 rpm at 20 °C in a Beckman SW41 rotor. 0.5 ml fractions were collected using a needle pierced through the bottom of the centrifuge tube. An aliquot of these fractions was analyzed on a 0.7% agarose gel. The fractions containing DNA molecules with a size of $\gg 20$ kb were pooled and concentrated by ethanol precipitation.

Subsequently, the cohesive ends were partially filled-in with dATP and dGTP using the strategy of partial filling of 5'-extensions of DNA produced by type II restriction endonuclease as described by Korch (1987, Nucleic Acids Res. **15**, 3199-3220) and Loftus *et al.* (1992, Biotechniques **12**, 172-176).

The binary cosmid vector pJJ04541 was digested completely with *XhoI* and the linear fragment was partially filled-in with dTTP and dCTP as described by Korch (1987, Nucleic Acids Res. **15**, 3199-3220).

The 20-kb fragments were ligated to the cosmid vector and transduced to *E. coli* strain XL1-Blue MR (Stratagene, La Jolla, CA, USA) using phage lambda Gigapack II XL packaging extracts (Stratagene, La Jolla, CA, USA) as recommended by the manufacturers. Selection was performed on LB (1% bacto-tryptone, 0.5% bacto-yeast extract and 1% NaCl, pH 7.5) agar plates containing 10 mg/l of tetracyclin. A bank of approximately 250.000 cosmid clones was made from 2-3 mg of size fractionated yeast DNA.

Subsequently, these transformants were stored into the wells of microtiter plates (96-wells, 100 μ l of LB medium containing 10 mg/l of

tetracyclin). Replicas of the 96-well grid of cosmid clones in microtiter plates were stamped onto Gene Screen Plus membrane filters (DuPont NEN, Boston, MA, USA) and allowed to grow into colonies on media. Colony hybridization using ^{32}P -labelled *SgrA1* fragment revealed positive cosmids. Of about 10.000 colonies approximately 150 positive cosmid clones were identified.

EXAMPLE 7: DETAILED PHYSICAL MAP OF THE 255 *SgrA1* FRAGMENT AND LOCATION OF THE AFLP MARKERS

Construction of a cosmid contig of the 255 kb *SgrA1* fragment

Standard techniques for growth and manipulation of cosmids in *E. coli* were followed (Sambrook *et al.* in Molecular cloning: a laboratory manual, 1989, Cold Spring Harbor Laboratory Press). Cosmid DNA was isolated by alkaline lysis using the method as described by Ish-Horowicz *et al.* (1981, Nucl. Acids Res. 9, 2989-2997). Approximately 500 ng was used for template preparation and the primers in the amplification of restriction fragments were the *EcoRI*-primer 5'-GACTGCGTACCAATTC-3' having no selective nucleotide and the *MseI*-primer 5'-GATGAGTCCTGAGTAA-3' having no selective nucleotide as described in Example 2. The *EcoRI*-primer was labelled at the 5' end and each of the 150 DNAs was amplified using the described primer set. The DNA fingerprints contained about 8 to 20 amplified fragments. Sets of DNA samples containing amplified fragments of identical size were selected and were rerun on polyacrylamide gels as described in Example 2 until a contiguous array of all the amplified fragments throughout the *SgrA1* fragment was obtained. The final fingerprint of the cosmid contig is shown in Figure 3.

Restriction fragment amplification is an excellent tool for contig building of cosmids, however the level of overlap between two adjacent cosmids cannot be determined using the enzyme combination as described above. Therefore, the DNA samples of the cosmid contig were digested with *EcoRI* and *HindIII* followed by Southern blot analysis according to Southern,

J. Mol. Biol. **98**, 503-515. ³²P-labelled *SgrAI* fragment was used as a probe and the sizes of the overlapping fragments between two adjacent cosmid DNAs was determined making use of size markers. Adjacent cosmids having an overlap of at least 5 kb were used for complementation analysis.

5

Fine mapping of the 18 AFLP markers on the 255 kb *SgrAI* fragment

The indirect end-label mapping technique as described by Burke *et al.* (1987, Science **236**, 806-812), for the restriction enzymes *MluI* and *SaII* and using the left-end probe (see described in example 5) was performed to
10 construct a more precise physical map of the 255 kb *SgrAI* fragment containing the *I-2* resistance gene. Pulse field gel electrophoresis was performed under conditions that maximise resolution in the range up to 100 kb.

To position the AFLP markers EM01 to EM18 on the physical map of
15 the 255 kb *SgrAI* fragment two types of hybridization analysis were performed. First, the AFLP markers were used as probes on the *MluI* and *SaII* partial digests and secondly the AFLP markers were used as probes on DNAs of the cosmid contig using standard hybridization techniques as described by Sambrook *et al.* (in Molecular cloning: a laboratory manual,
20 1989, Cold Spring Harbor Laboratory Press).

A physical fine map for the enzymes *MluI* and *SaII* of the *SgrAI* fragment and the position of the 18 AFLP markers EM01 to EM18 is shown in Figure 4.

25 **EXAMPLE 8: TRANSFORMATION**

Transfer of cosmids to *Agrobacterium tumefaciens*

The cosmid clones were introduced in *Agrobacterium tumefaciens* through conjugative transfer in a tri-parental mating with helper strain HB101 (pRK2013) essentially according to Deblaere *et al.* (1987, Methods in
30 Enzymology **153**, 277-292). *E.coli* were grown in LB medium (1% bacto-tryptone, 0.5% bacto-yeast extract and 1% NaCl, pH 7.5) supplemented with

5 mg/l tetracyclin at 37°C. The helper strain HB101 (pRK2013) was grown under identical conditions in LB medium supplemented with 100 mg/l kanamycin sulphate. *Agrobacterium tumefaciens* strain C58C1Rif^R (pGV3101) (Van Larebeke *et al.*, 1974, Nature, 252, 169-170) was grown in LB medium supplemented with 100 mg/l rifampicin at 28°C.

Overnight cultures were collected by centrifugation at 4000 r.p.m. for 5 min and resuspended in LB medium without any supplements, and 0.5 ml each of the *Agrobacterium* culture, the helper strain culture and a cosmid strain culture were mixed and plated on LB agar plates without antibiotics. After overnight incubation at 28°C, the mixture was plated on LB agar plates containing 100 mg/l rifampicin and 5 mg/l tetracyclin to select for single transconjugant *Agrobacterium* colonies in serial passages through selective agar plates.

Characterization of *A. tumefaciens* transconjugants

Small-scale cultures were grown from selected colonies and grown in LB medium containing 10 mg/l tetracyclin. Plasmid DNA was isolated by alkaline lysis using the method as described by Ish-Horowicz *et al.* (1981, Nucl. Acids Res. 9, 2989-2997). and digested with *Bgl*II using standard techniques. In addition, restriction fragment amplification on miniprep DNA of *A. tumefaciens* was performed using the enzyme combination *Eco*RI/*Mse*I and primers having no selective nucleotide as described in Example 7. Subsequently, the *Bgl*III restriction enzyme pattern as well as the DNA fingerprint of the *A. tumefaciens* transconjugant were compared with those of miniprep DNA of the *E. coli* strain containing the cosmid. Only those *A. tumefaciens* transconjugants harbouring a cosmid with the same DNA pattern as the corresponding *E. coli* culture were used to transform a susceptible tomato line.

Transformation of a susceptible tomato line

Seeds of the susceptible tomato line 52201 (Rijk Zwaan) were surface-sterilized in 2% sodium hypochlorite for 10 min, rinsed three times in sterile distilled water, and placed on germination medium (consisting of half-strength MS medium according to Murashige and Skoog (1962, *Physiol. Plant.* **15**, 473-497), with 1% (w/v) sucrose and 0.8% agar) in glass jars or polypropylene culture vessels. They were left to germinate for 8 days. Culture conditions were 25°C, a photon flux density of 30 mmol.m⁻².s⁻¹ and a photoperiod of 16 /24 h.

Transformation of tomato was performed according to Koornneef *et al.* (1987, In: *Tomato Biotechnology*, 169-178, Alan R. Liss, Inc.), and is described briefly below. Eight day old cotyledon explants were precultured for 24 h in Petri dishes containing a feeder layer of *Petunia hybrida* suspension cells plated on MS20 medium (culture medium according to Murashige and Skoog (1962, *Physiol. Plant.* **15**, 473-497) with 2% (w/v) sucrose and 0.8% agar) supplemented with 10.7 mM α -naphthaleneacetic acid and 4.4 mM 6-benzylaminopurine. The explants were then infected with the diluted overnight culture of *Agrobacterium tumefaciens* containing the cosmid clone AA12, DD2, CC14, A52, B22, A55, CC16, A44, A29, CC3, AA2, AA9, BB8 or the cosmid vector pJJ04541 for 5-10 min, blotted dry on sterile filter paper and cocultured for 48 h on the original feeder layer plates. Culture conditions were as described above. Overnight cultures of *Agrobacterium tumefaciens* were diluted in liquid MS20 medium (medium according to Murashige and Skoog (1962, *Physiol. Plant.* **15**, 473-497), with 2% (w/v) sucrose, pH 5.7) to an O.D.₆₀₀ of 0.8.

Following the cocultivation, the cotyledon explants were transferred to Petri dishes with selective medium consisting of MS20 supplemented with 4.56 mM zeatin, 67.3 mM vancomycin, 418.9 mM cefotaxime and 171.6 mM kanamycin sulphate, and cultured under the culture conditions described above. The explants were subcultured every 3 weeks onto fresh medium. Emerging shoots were dissected from the underlying callus and transferred to

glass jars with selective medium without zeatin to form roots. The formation of roots in a medium containing kanamycin sulphate was regarded as an indication of the transgenic nature of the shoot in question. Truly transgenic regenerants were propagated *in vitro* by subculturing the apical meristem and auxiliary buds into glass jars with fresh selective medium without zeatin.

Seed production

Of every individual transformant, one or two clones were kept *in vitro*, while the remaining shoots were potted in soil, hardened off in a relative humidity >85% at 20 °C and a photoperiod of 16/24h for 7-10 days, and transferred to the greenhouse for seed production. Mature tomato plants were grown at 25-32 °C in a ventilated greenhouse with supplementary illumination from Sun-T lamps (Philips, Eindhoven, The Netherlands). They were watered daily, treated against mildew and *Trialeurodes* infestation and vibrated to ensure good seed set when flowering. Mature fruits were harvested, the seeds extracted, cleaned in 1% HCl for 1 h, rinsed with water and dried.

EXAMPLE 9: COMPLEMENTATION ANALYSIS

Identification of cosmids with the resistance gene by screening for resistance in transformed plants

The transformed plants (R_0 plants) of the transformation experiments were grown in the greenhouse for seed set as described in Example 8. For each of the cosmids AA12, DD2, CC14, A52, B22, A55, CC16, A44, A29, CC3, AA2, AA9, BB8 or pJJ04541 twenty R_0 plants were grown. R_1 lines of at least nine R_0 plants of each cosmid were tested for disease symptoms, except for pJJ04541 in which case four plants were tested, in order to identify cosmids with the *I-2* resistance gene. Twenty to 25 seedlings of each R_1 line were inoculated and evaluated as described in Example 1. In total 144 R_1 lines of the above mentioned 14 different cosmid transformations have been tested; 13 cosmids contain tomato insert DNA and one cosmid, pJJ04541, is

without insert DNA. The results are shown in Table 2. 128 transgenic R_0 plants appeared susceptible, because their R_1 lines were completely or nearly completely (at least 80% of the seedlings) obviously diseased. Sixteen R_0 plants are resistant, because their R_1 lines were segregating. Most of the R_1 lines segregated in a ratio of about 3:1, resistant and susceptible seedlings. The remaining R_1 lines had a small number of susceptible seedlings (segregation ratios of 5:1 and 10:1), indicating the presence of more than one copy of the insert in the corresponding R_0 plants. The 16 resistant R_0 plants had been derived from transformations with one of the following cosmids: A52, B22 and A55; these three cosmids overlap with each other. These identified cosmids were used for further molecular analysis.

TABLE 2

cosmid	R_0 plants	
	resistant	susceptible
AA12	0	10
DD2	0	11
CC14	0	10
A52	4	7
B22	8	3
A55	4	9
CC16	0	15
A44	0	10
A29	0	11
CC3	0	10
AA2	0	9
AA9	0	10
BB8	0	9
pJJ04541	0	4

Molecular analysis of the transformed plants with a resistant phenotype

To demonstrate that the resistant phenotype of transgenic plants, which were transformed with one of the overlapping cosmids A52, B22 and A55, is determined by the genomic insert present in the various cosmids, an AFLP analysis with the AFLP markers EM04, EM06 and EM14 was performed. The AFLP markers EM14 and EM06 were positioned on plasmids A52 and B22 whereas EM06 and EM04 were positioned on cosmid A55 (see Figure 5)

DNA was isolated from young leaves of resistant as well as susceptible R_1 plants derived from a resistant R_0 plant, as described by Bernatzki and Tanksley (1986, Theor. Appl. Genet. **72**, 314-321). Selective restriction fragment amplification was performed with the primer combinations identifying the markers EM14 and EM06 for the R_0 plants transformed with cosmids A52 and B22 and with the primer combinations identifying the markers EM06 and EM04 for the R_0 plants transformed with cosmid A55. The DNA fingerprints obtained showed in both cases and for both markers the presence of the markers in the resistant plants and the absence of the markers in the susceptible plants indicating that the three identified overlapping cosmids A52, B22 and A55 contain the *I-2* resistance gene.

EXAMPLE 10: PHYSICAL MAP OF THE OVERLAPPING COSMID CLONES CONTAINING THE *I-2* RESISTANCE GENE

Since the size of the cosmid inserts is within the range of 13-24 kb, standard techniques such as single, double and partial digestion analysis with restriction enzymes which are present in the polylinker sequence of the cosmid vector were performed as described by Sambrook *et al.* (in: Molecular cloning: a laboratory manual, 1989, Cold Spring Harbor Laboratory Press). A physical map of cosmid A52, B22 and partially A55, was constructed and the overlap between the three cosmids giving rise to a resistant phenotype (A52, B22 and A55) with respect to the adjacent cosmid clone CC16 revealing a susceptible phenotype, was determined and is depicted in Figure 5.

The insert size in cosmids A52 and B22 could be calculated and amount 23 and 17 kb, respectively. It appeared that the plant insert of cosmid B22 completely fits within cosmid A52. The minimal DNA segment containing the *I*-2 resistance gene was defined by the left-end of cosmid A55 until the right-end of cosmid B22 encompassing a region of approximately 8 kb in size.

EXAMPLE 11: NUCLEOTIDE SEQUENCE AND DEDUCED AMINO ACID SEQUENCE OF THE *I*-2 RESISTANCE GENE

Various fragments of the 8 kb DNA segment of cosmid B22 were subcloned into the *E. coli* vector pBluescript (Stratagene, La Jolla, CA, USA) using standard techniques as described by Sambrook *et al.* (in: Molecular cloning: a laboratory manual, 1989, Cold Spring Harbor Laboratory Press) and used for sequence analysis making use of the Pharmacia Autoread Sequencing Kit and the Pharmacia LKB A.L.F. DNA Sequencer device (Pharmacia LKB, Uppsala, Sweden). The nucleotide sequence of 6.5 kb ranging from approximately 600 nucleotides upstream of a *Hind*III site until the 3' end of cosmid B22 was determined and is shown in Figure 6. A large open reading frame of 3798 nucleotides encoding a protein of 1266 amino acids could be deduced.

CLAIMS

5 1. A nucleic acid whose DNA sequence is at least part of the DNA sequence provided in figure 6 or any DNA sequence homologous thereto.

2. The nucleic acid of claim 1 wherein said DNA sequence homologous to the DNA sequence of figure 6 is capable, when transferred to a host plant also liable of being rendered resistant by the DNA sequence of figure 6, of also rendering it resistant to *Fusarium* 2.

10 3. A nucleic acid according to claim 1 wherein said DNA sequence corresponds to a coding sequence starting at nucleotide 1798 and ending at nucleotide 5535 or any DNA sequence homologous thereto.

15 4. A nucleic acid according to claim 1 wherein said DNA sequence corresponds to a promoter sequence located 5' upstream of nucleotide 1797 or any DNA sequence homologous thereto.

5. A recombinant DNA construct comprising a nucleic acid according to any of claims 1-4.

20 6. A recombinant DNA construct in which said nucleic acid is under the control of a promoter recognized by the polymerases of the cells of a plant cell, said promoter being either endogenous or exogenous to said plant, and effective to control transcription and expression of said DNA sequence in such plant cells.

7. A vector suitable for transforming plant cells comprising a DNA construct according to claim 5 or 6.

25 8. Plasmid pKGI2-B22 as deposited under number CBS 546.95.

9. Bacterial cells comprising a vector or plasmid according to any of claims 7 or 8.

10. Recombinant plant genome comprising, incorporated therein, a DNA construct according to claim 5 or 6.

30 11. Plant cells comprising a DNA construct according to claim 5 or 6.

12. Plant comprising plant cells according to claim 11.

13. Seed comprising a DNA construct according to claim 5 or 6.

14. The recombinant plant genome of claim 10, in a plant cellular environment.

5 **15.** Process for obtaining plants having reduced susceptibility to fungi, comprising the following steps:

 i) inserting into the genome of a plant cell a DNA construct according to claim 5 or 6,

 ii) obtaining transformed plant cells,

10 iii) regenerating from said transformed plant cells genetically transformed plants, and

 iv) optionally, propagating said plants.

16. Process for protecting plants in cultivation against fungal infection, which comprises:

15 i) providing the genome of plants with a DNA construct according to claim 5 or 6, and

 ii) growing said plants.

17. Process for isolating a nucleic acid according to claim 1-4, comprising the following steps:

20 i) screening a genomic or cDNA library of a plant with a DNA sequence according to any of claims 1-4,

 ii) identifying positive clones which hybridize to said DNA sequence,

 iii) isolating said positive clones.

25 **18.** The process of claim 17 wherein said cDNA library originates from a first plant and the nucleic acid sought to be isolated belongs to a second plant.

19. Process for isolating a nucleic acid according to any of claims 1-4 using primer combinations identifying at least one of the AFLP markers EM01 to EM18.

30 **20.** Process for isolating a nucleic acid according to claim 19 wherein said primer combination identifies AFLP marker EM06.

21. An oligonucleotide comprising a DNA sequence which corresponds to at least part of the nucleic acid according to any of claims 1-4.

22. The oligonucleotide of claim 21, which is of a size sufficient to hybridize selectively to the DNA sequence of any of claims 1 to 4, yet not to other DNA sequences contained in a plant genome under stringent hybridizing conditions.

23. An oligonucleotide according to claim 21 wherein said DNA sequence corresponds to the sequence starting at nucleotide 3470 and ending at nucleotide 3565.

24. An oligonucleotide according to claim 21 wherein said DNA sequence is located at the 3'end, and preferably corresponds to the sequence 5'-AATTCAGA-3', which can prime the synthesis of DNA.

25. An oligonucleotide according to claim 21 wherein said DNA sequence is located at the 3'end, and preferably corresponds to the sequence 5'-TAATCT-3' which can prime the synthesis of DNA.

26. A primer combination comprising a first oligonucleotide according to claim 24 and a second oligonucleotide according to claim 25.

27. Diagnostic kit comprising at least one oligonucleotide according to any of claims 21-25.

28. Diagnostic kit comprising a primer combination according to claim 26.

29. Process for detecting the presence or absence of a DNA sequence according to any of claims 1-4, particularly in a plant DNA using a diagnostic kit according to claim 27.

30. A polypeptide having an amino acid sequence having the sequence provided in figure 6 or coded by the corresponding homologous sequence according to claim 1 or 2.

31. Process for the identification of elicitor molecules using the polypeptide according to claim 30 as a receptor molecule.

32. A RNA having the ribonucleotidic sequence of a transcript of part or all of the DNA sequence of claim 1 or 2.

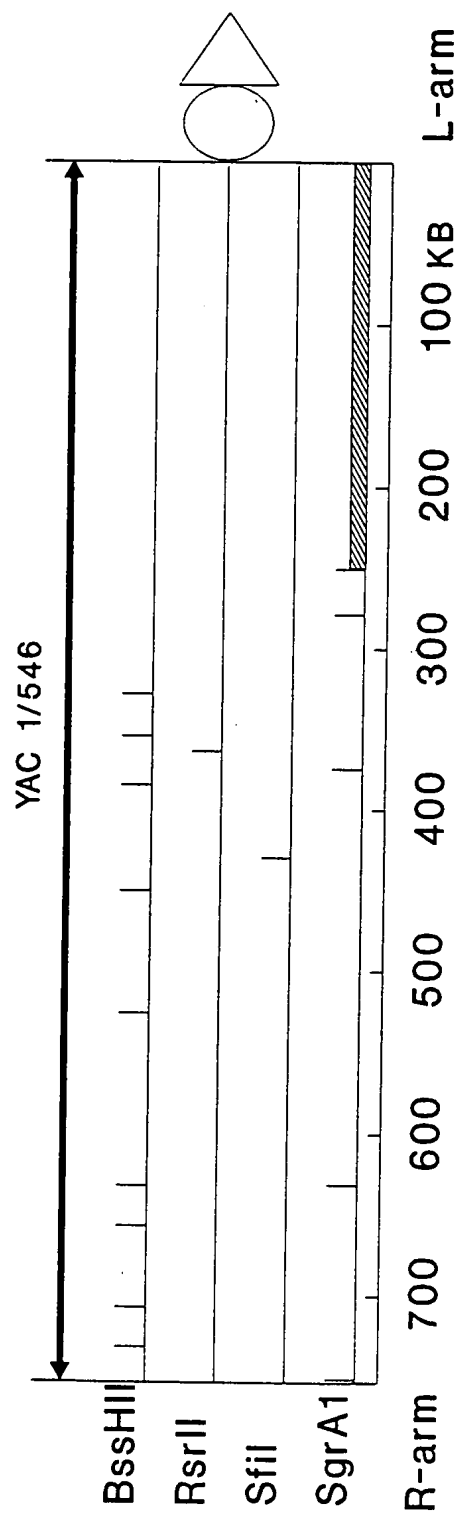


FIGURE 1

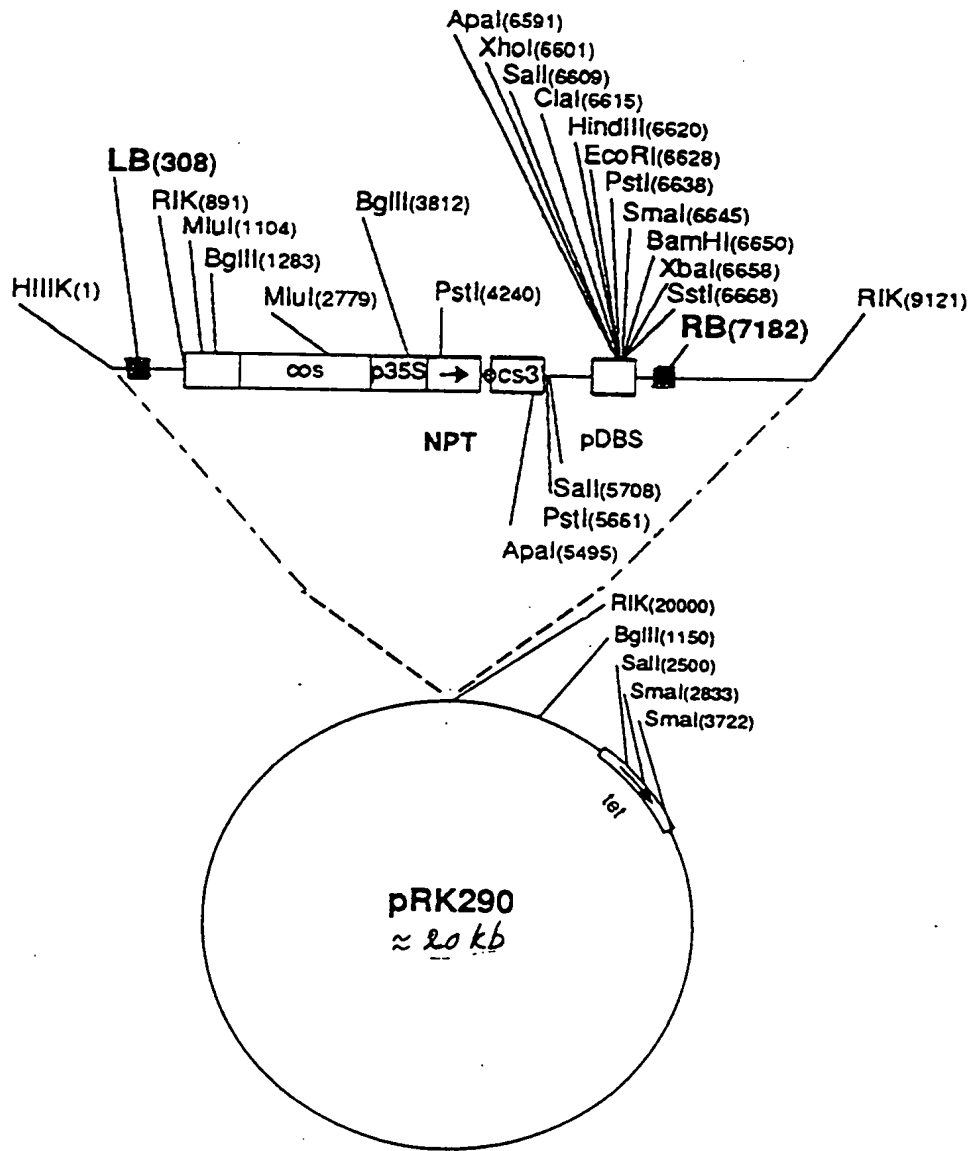


FIGURE 2

- 1 = B56
- 2 = A31
- 3 = A30
- 4 = B38
- 5 = CC13
- 6 = B31
- 7 = AA12
- 8 = DD2
- 9 = CC14
- 10 = A52
- 11 = B22
- 12 = A65
- 13 = A25
- 14 = A55
- 15 = CC16
- 16 = A44
- 17 = A29
- 18 = E20
- 19 = E4
- 20 = E15
- 21 = AAS
- 22 = E22
- 23 = CC3
- 24 = AA2

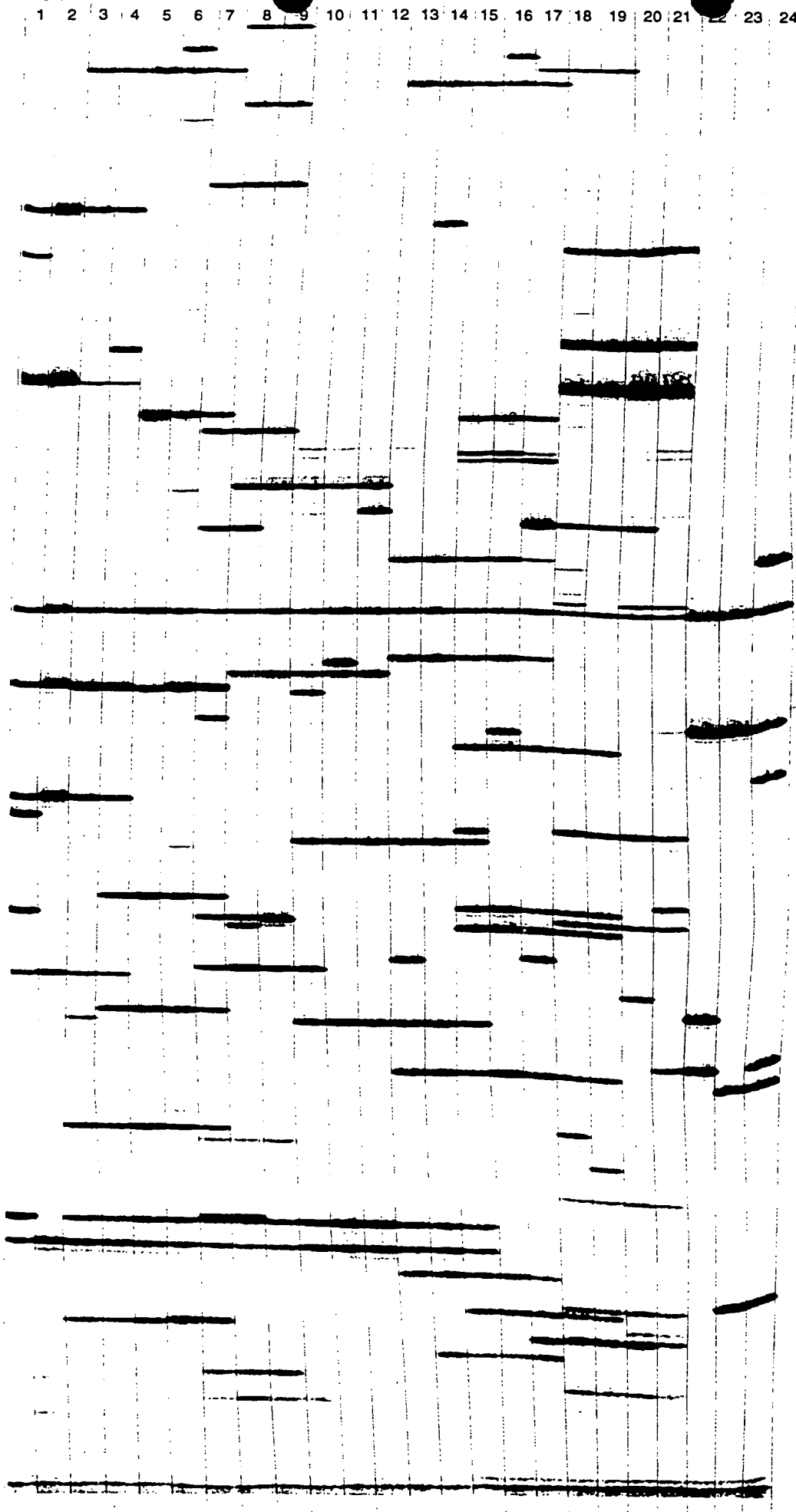


FIGURE 3

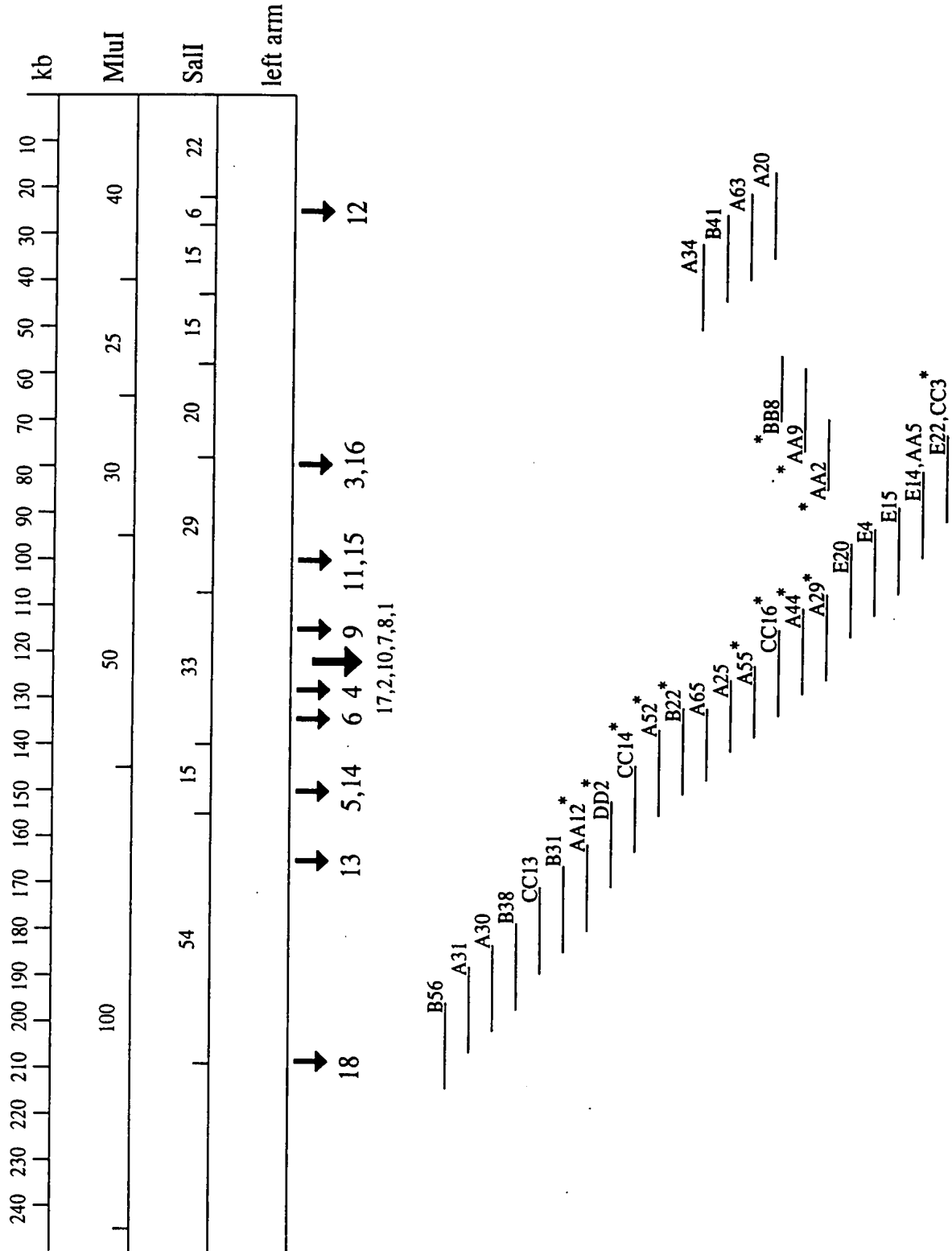


FIGURE 4

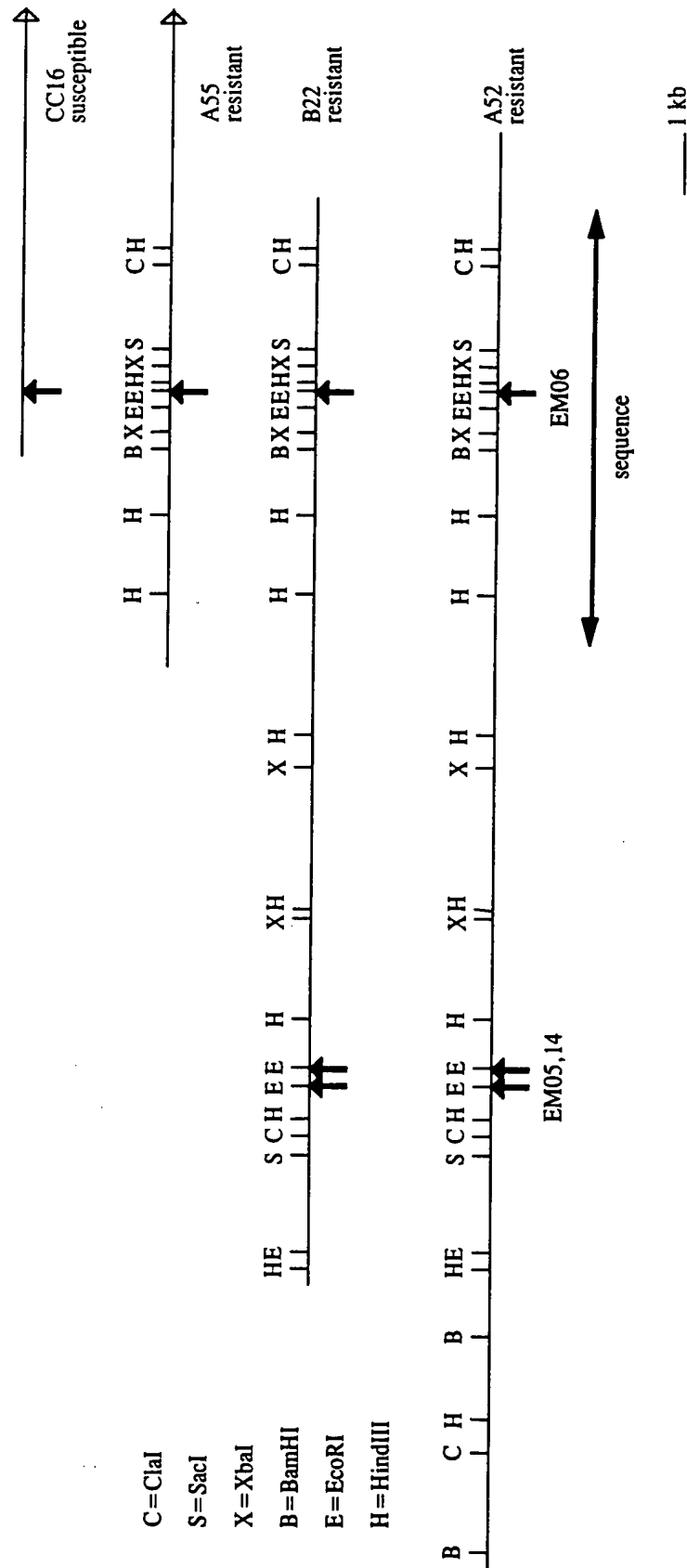


FIGURE 5

5' -AAAAAAGCAGCTTTAAAAAAGTACTTTKGAAAGGKGCTGAAACTTATTTTTTTGAAATAA 60
 GCAGTTATGTGTTTGGAAWAAAAGTGCTGAAGTTGCTATGTCAAACATGAAAAGGGRAAA 120
 AATGGAAGAAAGAGWTGTTAGGGTTATGTCGTAATTTGGAGATTGTATAAAAAATATTAAG 180
 GGCAAAAAAATAAAAAATGTGTCAACTTAAAACAGCTTATAAGCTAAAAGTTAAAAGCTG 240
 GGGTAGAGGTGTTTTTTTTTTTTTTAGCTTATAAGTTGTTTTAAGTTGACCACATTTTTTA 300
 TTTTTKTTGCCCTTAATATTTTTTATACAATCTCAAATTACGACATAACCCTAACATCTT 360
 TTTCTCCCATTTTTTCCTTTTCACGTTTGACATAGCAACTTCAGCACTTTTATCCAAACA 420
 CATAACTGCTTATTTTAAAAATAAGTTTCAGCACTTTCAAAAGTACTTTTTTAAAGCTGC 480
 TTTTATTAAGCCCATCCAAACGGGCCCTAAAATTGCTAATGTTTGCTCTTTCTATTCTCA 540
 AACTCCGTAATATTTAAGAAAATTTGCTAATGATAGGTCACTTTTAACACTAAATAATTA 600
 TAAATTGGGTAGAAATTTATTTTATCATTTTAAAGCTTTTTTAATTTTGAGTCTTCTCCCTA 660
 ATTAAGACCCCTCCCTCTTGCTTCAATTATTAAGTCAATAGTCTTTGTCTTATTGTTG 720
 GGTGAAAGTCTGTCTTCTTGTTAGGTACTAAGTCCTACAATAATATCAATAATTTGCTAT 780
 GGAGAAAAAATATTATAGGAGAAAAATAATTAATTTTAATTCATGAATATGTCTTAATA 840
 TGCAACTCATTTTGCTTATATATATCAAATTAAACTCTGTTCTTTAACTTTTTCTTATG 900
 AAGATACATTTTAAATTTATTTGATGAGGTTAGTTTTGAAATTTATATTATAATAATGAAA 960
 TGATATAACTTAAAAGAAGTTGTTTGATATCTTATCAGAATCATGCAGGTACTCATAATA 1020
 TAAGAAATAATTATGATGAAATTTATATATGTTTTATGCAGAGATTTATTACGCATTGTT 1080
 TACTTGGGTTATGTATTACTTATTTTCATCTTTTATCAGAATGTAAAATTATCATTCAATA 1140
 AGAAATCCAATTCTGTAAATTCAAATAACAACAATAACATTTTCAAGACCGATTTTTTT 1200
 NCCCAAGAATATACAGTAAACATATTTATGATATGGTAGGYCTCTTTAGTAATTGACCAM 1260
 CAAGGWTGTS GTGGAGTGGGAAATACTCTTTAATACTYCACCAAGAGGYCTCCAATTTG 1320
 AGCCCCTGAATACGAAATCGTCTTTGTAGTATATACCCTAACCTAATACAAAAAYTAGT 1380
 ATATTAGCCTTNACAGCTAAAATCTTTGTGACCTGTAAGTCACGCGAGGMCAAATTTACC 1440
 GTAACACCAACTTATYCATGATATAATTGTCCCTTTTAGCACGGTAATAATGAGGTGGGT 1500
 AGAAATTTATTACTTGAGGGCCCTTTCTACACCCACCCTTATTCTCTTGCTTCAATTATT 1560
 GAATTGAAGAAGTAATGAAAAANCAGACTCCATTGGATAAAGGACAGTTTGCAAACACAG 1620
 CTGTAACAATTTAGAGCACTAGCAAAATAGAGAGAGTTTGTGAGAGAAATTTTGTGTTGCA 1680
 AATTACTCTTAACCTTCAGCAGGTAAAATAAAGTTCTTAAGTACTGAGACTATTTGAAGATAT 1740
 ATTTTGTAAAGAATCATTTTGTGTGTTTCCTTGTTTTGCTTTTGCAGATTTGAGAAATG 1800
 M 1
 GAGATTGGCTTAGCAGTTGGTGGTGCATTTCTCTCCTCAGCTTTGAATGTTCTGTTTGAT 1860
 E I G L A V G G A F L S S A L N V L F D 21
 AGGCTTGCTCCTAACGGTGATCTGCTCAACATGTTTCGGAAGCATAAGGATCATGTTAAG 1920
 R L A P N G D L L N M F R K H K D H V K 41
 CTCTTAAAGAAGCTGAAAATGACTTTGCGTGTTATTCAGATTGTGCTAAGTGATGCAGAG 1980
 L L K K L K M T L R G I Q I V L S D A E 61
 AATAAGCAAGCATCAATCCATCTGTGAGAGACTGGCTTAATGAGCTTCGAGATGCTGTC 2040
 N K Q A S N P S V R D W L N E L R D A V 81
 GACTCTGCTGAAAATTTAATAGAAGAAGTCAATTATGAAGCTTTGAGGCTTAAGGTGGAA 2100
 D S A E N L I E E V N Y E A L R L K V E 101
 GGTCAGCATCAATTTTTCAGAAACAAGCAACCAGCAAGTAAGTGATGATTTTTTCCTT 2160
 G Q H Q N F S E T S N Q Q V S D D F F L 121
 AACATAAAGGACAAGCTGGAAGACACTATTGAACATTAAAGGATTTGCAAGAGCAAATT 2220
 N I K D K L E D T I E T L K D L Q E Q I 141
 GGTCTCCTTGCTTAAAGGAGTATTTTGATTCCACGAAACTAGAACTAGAAGACCTTCA 2280
 G L L G L K E Y F D S T K L E T R R P S 161
 ACTTCTGTGGATGATGAATCTGATATCTTTGGTAGGCAGAGCGAAATAGAGGATTTGATT 2340
 T S V D D E S D I F G R Q S E I E D L I 181
 GACCGTCTATTGTCTGAAGGTGCAAGTGGGAAAAAGCTGACAGTAGTTCCTATCGTTGGA 2400
 D R L L S E G A S G K K L T V V P I V G 201
 ATGGGCGGCCAGGGCAAGACAACACTTGCTAAAGCCGTATACAATGATGAGAGGGTGAAG 2460
 M G G Q G K T T L A K A V Y N D E R V K 221
 AATCATTTTGATTTGAAAGCGTGTTGCTTTCTGAAGGATTTGATGCTTTGAGAATA 2520
 N H F D L K A W Y C V S E G F D A L R I 241
 ACAAAGAATTACTCCAAGAAATTTGGCAAATTTGACTCGAAGGATGTCCACAACAATCTT 2580
 T K E L L Q E I G K F D S K D V H N N L 261

FIGURE 6a

AACCAGCTTCAAGTCAAATTGAAGGAAAGTTTGAAGGGAAAGAAGTTCCTTATTGTTTTG 2640
 N Q L Q V K L K E S L K G K K F L I V L 281
 GATGATGTGTGGAATGAAAATTACAACGAGTGGAATGACTTGAGAAATATTTTGCACAA 2700
 D D V W N E N Y N E W N D L R N I F A Q 301
 GGAGATATAGGAAGTAAGATCATTGTGACGACACGCAAAGACAGTGTTCCTTGATGATG 2760
 G D I G S K I I V T T R K D S V A L M M 321
 GGAAATGAGCAAATTCGCATGGGCAATTTGTCTACCGAAGCCTCTTGGTCTTTATTTCAA 2820
 G N E Q I R M G N L S T E A S W S L F Q 341
 AGACATGCATTTGAAAACATGGATCCTATGGGACATCCGGAACCTTGAAGAGGTCGGAAGA 2880
 R H A F E N M D P M G H P E L E E V G R 361
 CAAATTGCAGCCAAGTGCAAAGGACTGCCCTTAGCTCTGAAGACGCTCGCTGGCATGTTA 2940
 Q I A A K C K G L P L A L K T L A G M L 381
 CGCTCCAAATCAGAGGTTGAAGAGTGGAACGTATTTTGAGAAGTGAATATGGGAGCTG 3000
 R S K S E V E E W K R I L R S E I W E L 401
 CCACACAATGACATATTACCAGCGTTGATGTTGAGCTACAATGATCTTCCCGCACATTTA 3060
 P H N D I L P A L M L S Y N D L P A H L 421
 AAGCGATGCTTTTTCTTTTGTGCAATATTTCTTAAAGATTATCCATTTAGGAAAGAACAA 3120
 K R C F S F C A I F P K D Y P F R K E Q 441
 GTTATTTCATCTATGGATTGCCAATGGTCTCGTACCAGTGAAAGATGAAATAAATCAAGAT 3180
 V I H L W I A N G L V P V K D E I N Q D 461
 TTAGGCAACCAATACTTTCTAGAGTTGAGATCAAGATCATTATTTGAAAAGGTCCCAAAT 3240
 L G N Q Y F L E L R S R S L F E K V P N 481
 CCTTCTAAAAGGAACATAGAGGAATTATTCCTTATGCATGACCTTGTCAATGATTTAGCC 3300
 P S K R N I E E L F L M H D L V N D L A 501
 CAACTTGCATCTTCAAAACTTTGTATCAGGTTAGAAGAGAGCCAAGGATCTCATATGTTG 3360
 Q L A S S K L C I R L E E S Q G S H M L 521
 GAACAATGTCGGCACTTATCTTATTCAATAGGATTTAATGGTGAGTTTAAGAAATTGACA 3420
 E Q C R H L S Y S I G F N G E F K K L T 541
 CCCCTCTACAAATTGGAGCAGTTGAGGACATTGCTTCCGATACGTATTGAATTGAGATTG 3480
 P L Y K L E Q L R T L L P I R I E F R L 561
 CACAATCTAAGCAAGAGGGTGTTCATAACATACTGCCTACACTAAGATCCTTGAGGGCC 3540
 H N L S K R V L H N I L P T L R S L R A 581
 CTATCATTCTCTCAATACAAGATTAAGGAGTTGCCAAATGACTTGTTTACCAAATTAAAG 3600
 L S F S Q Y K I K E L P N D L F T K L K 601
 CTCCTCAGATTTTTGGATATTTCTCGGACATGGATTACAAAGTTGCCGGATTCCATTTGT 3660
 L L R F L D I S R T W I T K L P D S I C 621
 GGATTATATAACTTGGAGACACTTCTCCTGTCTATCTTGTGCTGATCTTGAGGAGCTACCG 3720
 G L Y N L E T L L L S S C A D L E E L P 641
 CTGCAGATGGAGAAGTTGATTAAGTTCGCTCATCTTGACGTAAGCAACACTCGGCGCTTG 3780
 L Q M E K L I N L R H L D V S N T R R L 661
 AAGATGCCACTACATCTGAGCAGGTTGAAAAGCCTCCAAGTGTTGGTGGGACCCAAGTTT 3840
 K M P L H L S R L K S L Q V L V G P K F 681
 TTTGTAGATGGTTGGAGAATGGAAGATTTGGGTGAAGCACAAAACCTTACATGGATCTCTA 3900
 F V D G W R M E D L G E A Q N L H G S L 701
 TCAGTTGTGAAGTTGGAAAATGTGTTGATAGAAGGGAAGCTGTGAAGGCAAAGATGAGG 3960
 S V V K L E N V V D R R E A V K A K M R 721
 GAGAAGAATCATGTTGAGCAATTATCATTGGAGTGGAGTGAAAGTAGTATTGCCGACAAT 4020
 E K N H V E Q L S L E W S E S S I A D N 741
 TCACAAACAGAAAGTGACATACTTGATGAGCTATGCCACATAAAAACATCAAAAAAGTC 4080
 S Q T E S D I L D E L C P H K N I K K V 761
 GAAATCAGTGGATATAGAGGGACAAACTTTCCCAATTGGGTAGCTGATCCTTTGTTTCTT 4140
 E I S G Y R G T N F P N W V A D P L F L 781
 AAGCTGGTGAATTTGTCTCTAAGAACTGCAAGGACTGTTACTCCTTGCCAGCACTAGGA 4200
 K L V N L S L R N C K D C Y S L P A L G 801
 CAACTCCCTTGTTTGAATTCCTTTCCGTTAAAGGGATGCATGGAATAAGAGTGGTGACG 4260
 Q L P C L K F L S V K G M H G I R V V T 821

FIGURE 6b

GAAGAATTCTATGGCAGATTGTCCTCCAAAAAGCCTTTTAACTCTCTAGAGAAGCTTGAA 4320
 E E F Y G R L S S K K P F N S L E K L E 841
 TTTGAAGATATGACGGAGTGGAAGCAATGGCACGCACTAGGAATTGGAGAGTTCCTTACA 4380
 F E D M T E W K Q W H A L G I G E F P T 861
 CTTGAGAACCTTTCAATTAATAAATTGCCCCTGAGCTCAGTTTGGAGATACCCATCCAATTT 4440
 L E N L S I K N C P E L S L E I P I Q F 881
 TCAAGTTTAAAAAGGTTAGAAGTTAGTGATTGTCCAGTTGTTTTTGATGATGCCCAACTG 4500
 S S L K R L E V S D C P V V F D D A Q L 901
 TTTAGATCCCAACTTGAGGCAATGAAGCAGATTGAGGAAATAGATATATGTGATTGTAAC 4560
 F R S Q L E A M K Q I E E I D I C D C N 921
 TCTGTTACCTCCTTTTCCTTTTAGCATACTGCCAACTACCTTGAAGAGAATACAGATATCT 4620
 S V T S F P F S I L P T T L K R I Q I S 941
 CGTTGCCCAAAATTGAAATTGGAGGCGCCAGTTGGTGAGATGTTTGTGGAGTATTTGAGA 4680
 R C P K L K L E A P V G E M F V E Y L R 961
 GTGAATGATTGTGGTTGTGTAGATGATATATCACCTGAGTTTCTCCCAACAGCACGTCAA 4740
 V N D C G C V D D I S P E F L P T A R Q 981
 TTGAGTATTGAAAATTGCCAGAACGTTACTAGGTTTTTTGATTCTTACTGCCACTGAAACT 4800
 L S I E N C Q N V T R F L I P T A T E T 1001
 CTCCGTATTTTCGAATTGTGAGAATGTTGAAAACTATCGGTGGCATGTGGAGGAGCGGCC 4860
 L R I S N C E N V E K L S V A C G G A A 1021
 CAGATGACGTCACTGAATATTTGGGGATGTAAGAAGCTCAAGTGTCTTCCAGAACTCCTT 4920
 Q M T S L N I W G C K K L K C L P E L L 1041
 CCATCTCTCAAGGAACTGCGTCTGTCTGATTGTCCAGAAATAGAAGGAGAATTGCCCTTC 4980
 P S L K E L R L S D C P E I E G E L P F 1061
 AATTTAGAAATACTCCGTATCATATATTGCAAGAACTGGTGAATGGCCGAAAGGAGTGG 5040
 N L E A I L R I I Y C K K L V N G R K E W 1081
 CATTTACAGAGACTCACAGAGTTATGGATCGATCATGATGGGAGTGACGAAGATATTGAA 5100
 H L Q R L T E L W I D H D G S D E D I E 1101
 CATTGGGAGTTGCCTTGTTCTATTTCAGAGACTTACCATAAAGAATCTTAAACATTAAAGC 5160
 H W E L P C S I Q R L T I K N L K T L S 1121
 AGCCAACATCTCAAAAGCCTCACCTCTCTTCAATATCTATGTATTGAGGGTTATTTATCT 5220
 S Q H L K S L T S L Q Y L C I E G Y L S 1141
 CAGATTCAGTCACAAGGCCAGCTTTTCCTCCTTTTCTCACCTCACTTCGCTTCAAACCTCTA 5280
 Q I Q S Q G Q L S S F S H L T S L Q T L 1161
 CAAATCTGGAATTTCCCTTAATCTCCAATCACTTGCTGAATCAGCACTGCCCTCCTCCCTC 5340
 Q I W N F L N L Q S L A E S A L P S S L 1181
 TCTCACCTGGAGATAGATGATTGCCCTAATCTCCAATCACTCTTCAATCAGCACTGCC 5400
 S H L E I D D C P N L Q S L F E S A L P 1201
 TCCTCCCTCTCTCAGCTGTTTCATCCAGGATTGCCCTAATCTCCAATCCCTTCCATTAAA 5460
 S S L S Q L F I Q D C P N L Q S L P F K 1221
 GGGATGCCCTCTTCCCTCTCTAAACTATCTATTTTCAATTGCCCATTTGCTCACACCACTA 5520
 G M P S S L S K L S I F N C P L L T P L 1241
 CTAGAATTTGACAAGGGGGAATACTGGCCACAAATTGCTCATATTCCCATCATAAATATC 5580
 L E F D K G E Y W P Q I A H I P I N I 1261
 GATTGGAAATATATTTAAACAATTAAACAAATGGCTCTCCAACCTGATGTAAGCTATTTCGT 5640
 D W K Y I --- 1266
 TACCCTTAGAAGCTTTTTTATGATTCTATGTTTCTCATTGCTTATTGGTTTATGCTCTTAC 5700
 CGTGTTTTAAATTCACGTCTCAATTGCCACCATGTTTAAATCGAAAGTTTTTAGTTCTTGTA 5760
 ATCATCAACCATCCTATGTCACTAGAAATTTTGATAGGTAAAAGAGGTAGACAAAAAAGC 5820
 TAAACATCTTTTTTCTTTTCGTATAGCGACCAACAACACTACATTTTGTAGAGTAAGGGCTA 5880
 TAGATATACATTTGCAGGGTGTTAAACCAAGGAGTAAGAAAATCACTGTCTTCAGATATC 5940
 TTCTCTTGCAATATACTTTTGCAATTTTAAAGCTACATTTTGAAGCTCATGTGTTGTTGCTAA 6000
 CTTAAACATGTTTTGTGCTTAATCAGATGTGGATTTTGAAGAGCGAGTACGACAAGTCTG 6060
 GTACATTAATTGTCCGTAGAAGTGTTTCTAAGGTGCTGCTGCTATTTTTTACATCTGTTCC 6120
 CGAGTTTTGTTTTTTTTTTTAAATCTTTCCACTAAAGCTATTATGTCGTCCACAGTGAATT 6180
 TTCAGGTCTGTTGTTATAGGCAAGTCTTTGAGATGCGACTATCAAAGAAGGGCGATTACA 6240

FIGURE 6c

ATCAGTGTACCGCTGAAACTATTTTCATGTTTCCAGTGCAAGCCTCTTTTGTAAGTTGACA	6300
AACTCGATTAGTTAATATGTTTGGGACTCAACTAGTGGTTAGAGTACTCATTTTGTAAGA	6360
CTTGTGTACAGAAAATCAAATTAGAATTATAACTCGTGATGGTTGAATAAACTCTAAGAA	6420
GTAAGTATATATTTTTTAGTGGATATGTTGTTTGCTCATTTCGGTGGTTGATATCCACATT	6480
GGAGTCCAACTAAATTCGAATTTGCACAATCGAAGGAGCGGTGCTCCTGGCATGATTTTT	6540
TTCCCATTCTACGACTAGTGCTCCTAAATTCTAATTAAGCATAGAAAAATCTCAACTATC	6600
TCACCCAACTCATATCAGGATAGAGTATTCCTGAGGAGGATTCCTTCAGTTACAAA-3'	6658

FIGURE 6d